



(19) Europäisches Patentamt
European Patent Office
Office européen des brevets



(11) Publication number:

0 368 684 B1

(12)

EUROPEAN PATENT SPECIFICATION

- (45) Date of publication of patent specification: **09.03.94** (51) Int. Cl.⁵: **C07K 13/00, C12N 15/10,
C12N 15/13, //C12Q1/68**
(21) Application number: **89311731.7**
(22) Date of filing: **13.11.89**

(54) **Cloning immunoglobulin variable domain sequences.**

- (30) Priority: **11.11.88 GB 8826444
16.03.89 GB 8906034
22.04.89 GB 8909217
15.05.89 GB 8911047
02.06.89 GB 8912652
16.06.89 GB 8913900
15.08.89 GB 8918543**
(43) Date of publication of application:
16.05.90 Bulletin 90/20
(45) Publication of the grant of the patent:
09.03.94 Bulletin 94/10
(84) Designated Contracting States:
AT BE CH DE ES FR GB GR IT LI LU NL SE
(56) References cited:
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Description

The present invention relates to cloning of immunoglobulin (Ig) variable domain sequences. Methods for cloning, amplifying and expressing DNA sequences encoding at least part of an immunoglobulin variable 5 domain and methods for the use of said DNA sequences in the production of Ig-type molecules are disclosed.

A list of references is appended to the end of the description. The documents listed therein are referred to in the description by number, which is given in square brackets [].

The Ig superfamily includes not only the Igs themselves but also such molecules as receptors on 10 lymphoid cells such as T lymphocytes. Immunoglobulins comprise at least one heavy and one light chain covalently bonded together. Each chain is divided into a number of domains. At the N terminal end of each chain is a variable domain. The variable domains on the heavy and light chains fit together to form a binding site designed to receive a particular target molecule. In the case of Igs, the target molecules are antigens. T-cell receptors have two chains of equal size, the α and β chains, each consisting of two 15 domains. At the N-terminal end of each chain is a variable domain and the variable domains on the α and β chains are believed to fit together to form a binding site for target molecules, in this case peptides presented by a histocompatibility antigen. The variable domains are so called because their amino acid sequences vary particularly from one molecule to another. This variation in sequence enables the molecules to recognise an extremely wide variety of target molecules.

20 Much research has been carried out on Ig molecules to determine how the variable domains are produced. It has been shown that each variable domain comprises a number of areas of relatively conserved sequence and three areas of hypervariable sequence. The three hypervariable areas are generally known as complementarity determining regions (CDRs).

25 Crystallographic studies have shown that in each variable domain of an Ig molecule the CDRs are supported on framework areas formed by the areas of conserved sequences. The three CDRs are brought together by the framework areas and, together with the CDRs on the other chain, form a pocket in which the target molecule is received.

30 Since the advent of recombinant DNA technology, there has been much interest in the use of such technology to clone and express Ig molecules and derivatives thereof. This interest is reflected in the numbers of patent applications and other publications on the subject.

The earliest work on the cloning and expression of full Igs in the patent literature is EP-A-0 120 694 35 (Boss). The Boss application also relates to the cloning and expression of chimeric antibodies. Chimeric antibodies are Ig-type molecules in which the variable domains from one Ig are fused to constant domains from another Ig. Usually, the variable domains are derived from an Ig from one species (often a mouse Ig) and the constant domains are derived from an Ig from a different species (often a human Ig).

A later European patent application, EP-A-0 125 023 (Genentech), relates to much the same subject as the Boss application, but also relates to the production by recombinant DNA technology of other variations of Ig-type molecules.

EP-A-0 194 276 (Neuberger) discloses not only chimeric antibodies of the type disclosed in the Boss 40 application but also chimeric antibodies in which some or all of the constant domains have been replaced by non-Ig derived protein sequences. For instance, the heavy chain CH₂ and CH₃ domains may be replaced by protein sequences derived from an enzyme or a protein toxin.

EP-A-0 239 400 (Winter) discloses a different approach to the production of Ig molecules. In this approach, only the CDRs from a first type of Ig are grafted onto a second type of Ig in place of its normal 45 CDRs. The Ig molecule thus produced is predominantly of the second type, since the CDRs form a relatively small part of the whole Ig. However, since the CDRs are the parts which define the specificity of the Ig, the Ig molecule thus produced has its specificity derived from the first Ig.

Hereinafter, chimeric antibodies, CDR-grafted Igs, the altered antibodies described by Genentech, and fragments, of such Igs such as F(ab')₂ and Fv fragments are referred to herein as modified antibodies.

50 One of the main reasons for all the activity in the Ig field using recombinant DNA technology is the desire to use Igs in therapy. It is well known that, using the hybridoma technique developed by Kohler and Milstein, it is possible to produce monoclonal antibodies (MAbs) of almost any specificity. Thus, MAbs directed against cancer antigens have been produced. It is envisaged that these MAbs could be covalently attached or fused to toxins to provide "magic bullets" for use in cancer therapy. MAbs directed against normal tissue or cell surface antigens have also been produced. Labels can be attached to these so that they can be used for *in vivo* imaging.

The major obstacle to the use of such MAbs in therapy or *in vivo* diagnosis is that the vast majority of MAbs which are produced are of rodent, in particular mouse, origin. It is very difficult to produce human

MAbs. Since most MAbs are derived from non-human species, they are antigenic in humans. Thus, administration of these MAbs to humans generally results in an anti-Ig response being mounted by the human. Such a response can interfere with therapy or diagnosis, for instance by destroying or clearing the antibody quickly, or can cause allergic reactions or immune complex hypersensitivity which has adverse effects on the patient.

The production of modified Igs has been proposed to ensure that the Ig administered to a patient is as "human" as possible, but still retains the appropriate specificity. It is therefore expected that modified Igs will be as effective as the MAb from which the specificity is derived but at the same time not very antigenic. Thus, it should be possible to use the modified Ig a reasonable number of times in a treatment or diagnosis regime.

At the level of the gene, it is known that heavy chain variable domains are encoded by a "rearranged" gene which is built from three gene segments: an "unrearranged" VH gene (encoding the N-terminal three framework regions, first two complete CDRs and the first part of the third CDR), a diversity (DH)-segment (DH) (encoding the central portion of the third CDR) and a joining segment (JH) (encoding the last part of the third CDR and the fourth framework region). In the maturation of B-cells, the genes rearrange so that each unrearranged VH gene is linked to one DH gene and one JH gene. The rearranged gene corresponds to VH-DH-JH. This rearranged gene is linked to a gene which encodes the constant portion of the Ig chain.

For light chains, the situation is similar, except that for light chains there is no diversity region. Thus light chain variable domains are encoded by an "unrearranged" VL gene and a JL gene. There are two types of light chains, kappa (κ) or lambda (λ), which are built respectively from unrearranged $V\kappa$ genes and $J\kappa$ segments, and from unrearranged $V\lambda$ genes and $J\lambda$ segments.

It has been discovered that isolated Ig heavy chain variable domains can bind to antigen in a 1:1 ratio and with binding constants of equivalent magnitude to those of complete antibody molecules.

Single domain ligands consisting of at least part of the variable domain of one chain of a molecule from the Ig superfamily may be the end product of processes involving methods according to the present invention.

Preferably, each ligand consists of the variable domain of an Ig light, or, most preferably, heavy chain.

If desired, a gene for a single domain ligand can be mutated to improve the properties of the expressed domain, for example to increase the yields of expression or the solubility of the ligand, to enable the ligand to bind better, or to introduce a second site for covalent attachment (by introducing chemically reactive residues such as cysteine and histidine) or non-covalent binding of other molecules. In particular it would be desirable to introduce a second site for binding to serum components, to prolong the residence time of the domains in the serum; or for binding to molecules with effector functions, such as components of complement, or receptors on the surfaces of cells.

Thus, hydrophobic residues which would normally be at the interface of the heavy chain variable domain with the light chain variable domain could be mutated to more hydrophilic residues to improve solubility; residues in the CDR loops could be mutated to improve antigen binding; residues on the other loops or parts of the β -sheet could be mutated to introduce new binding activities. Mutations could include single point mutations, multiple point mutations or more extensive changes and could be introduced by any of a variety of recombinant DNA methods, for example gene synthesis, site directed mutagenesis or the polymerase chain reaction.

Since these ligands have equivalent binding affinity to that of complete Ig molecules, the ligands can be used in many of the ways as are Ig molecules or fragments. For example, Ig molecules have been used in therapy (such as in treating cancer, bacterial and viral diseases), in diagnosis (such as pregnancy testing), in vaccination (such as in producing anti-idiotypic antibodies which mimic antigens), in modulation of activities of hormones or growth factors, in detection, in biosensors and in catalysis.

It is envisaged that the small size of the ligands may confer some advantages over complete antibodies, for example, in neutralising the activity of low molecular weight drugs (such as digoxin) and allowing their filtration from the kidneys with drug attached; in penetrating tissues and tumours; in neutralising viruses by binding to small conserved regions on the surfaces of viruses such as the "canyon" sites of viruses [16]; in high resolution epitope mapping of proteins; and in vaccination by ligands which mimic antigens.

A single domain ligand may be linked to one or more of an effector molecule, a label, a surface, or one or more other ligands having the same or different specificity, forming a "receptor".

A receptor comprising a ligand linked to an effector molecule may be of use in therapy. The effector molecule may be a toxin, such as ricin or pseudomonas exotoxin, an enzyme which is able to activate a prodrug, a binding partner or a radio-isotope. The radio-isotope may be directly linked to the ligand or may be attached thereto by a chelating structure which is directly linked to the ligand. Such ligands with

attached isotopes are much smaller than those based on Fv fragments, and could penetrate tissues and access tumours more readily.

A receptor comprising a ligand linked to a label may be of use in diagnosis. The label may be a heavy metal atom or a radio-isotope, in which case the receptor can be used for *in vivo* imaging using X-ray or other scanning apparatus. The metal atom or radio-isotope may be attached to the ligand either directly or via a chelating structure directly linked to the ligand. For *in vitro* diagnostic testing, the label may be a heavy metal atom, a radio-isotope, an enzyme, a fluorescent or coloured molecule or a protein or peptide tag which can be detected by an antibody, an antibody fragment or another protein. Such receptors would be used in any of the known diagnostic tests, such as ELISA or fluorescence-linked assays.

10 A receptor comprising a ligand linked to a surface, such as a chromatography medium, could be used for purification of other molecules by affinity chromatography. Linking of ligands to cells, for example to the outer membrane proteins of *E. coli* or to hydrophobic tails which localise the ligands in the cell membranes, could allow a simple diagnostic test in which the bacteria or cells would agglutinate in the presence of molecules bearing multiple sites for binding the ligand(s).

15 Receptors comprising at least two ligands can be used, for instance, in diagnostic tests. The first ligand will bind to a test antigen and the second ligand will bind to a reporter molecule, such as an enzyme, a fluorescent dye, a coloured dye, a radio-isotope or a coloured-, fluorescently- or radio-labelled protein.

Alternatively, such receptors may be useful in increasing the binding to an antigen. The first ligand will bind to a first epitope of the antigen and the second ligand will bind to a second epitope. Such receptors 20 may also be used for increasing the affinity and specificity of binding to different antigens in close proximity on the surface of cells. The first ligand will bind to the first antigen and the second epitope to the second antigen: strong binding will depend on the co-expression of the epitopes on the surface of the cell. This 25 may be useful in therapy of tumours, which can have elevated expression of several surface markers. Further ligands could be added to further improve binding or specificity. Moreover, the use of strings of ligands, with the same or multiple specificities, creates a larger molecule which is less readily filtered from the circulation by the kidney.

For vaccination with ligands which mimic antigens, the use of strings of ligands may prove more effective than single ligands, due to repetition of the immunising epitopes.

If desired, such receptors with multiple ligands could include effector molecules or labels so that they 30 can be used in therapy or diagnosis as described above.

The ligand may be linked to the other part of the receptor by any suitable means, for instance by covalent or non-covalent chemical linkages. However, where the receptor comprises a ligand and another protein molecule, it is preferred that they are produced by recombinant DNA technology as a fusion product. If necessary, a linker peptide sequence can be placed between the ligand and the other protein 35 molecule to provide flexibility.

The basic techniques for manipulating Ig molecules by recombinant DNA technology are described in the patent references cited above. These may be adapted in order to allow for the production of single domain ligands and receptors by means of recombinant DNA technology.

Preferably, where the ligand is to be used for *in vivo* diagnosis or therapy in humans, it is humanised, 40 for instance by CDR replacement as described in EP-A-0 239 400.

In order to obtain a DNA sequence encoding a ligand, it is generally necessary firstly to produce a hybridoma which secretes an appropriate MAb. This can be a very time consuming method. Once an immunised animal has been produced, it is necessary to fuse separated spleen cells with a suitable myeloma cell line, grow up the cell lines thus produced, select appropriate lines, reclone the selected lines 45 and reselect. This can take some long time. This problem also applies to the production of modified Igs.

A further problem with the production of ligands, and also receptors described above and modified Igs, by recombinant DNA technology is the cloning of the variable domain encoding sequences from the hybridoma which produces the MAb from which the specificity is to be derived. This can be a relatively long method involving the production of a suitable probe, construction of a clone library from cDNA or 50 genomic DNA, extensive probing of the clone library, and manipulation of any isolated clones to enable the cloning into a suitable expression vector. Due to the inherent variability of the DNA sequences encoding Ig variable domains, it has not previously been possible to avoid such time consuming work. It is therefore a further aim of the present invention to provide a method which enables substantially any sequence encoding an Ig superfamily molecule variable domain (ligand) to be cloned in a reasonable period of time.

55 According to an aspect of the present invention therefore, there is provided a method of cloning a sequence (the target sequence) which encodes at least part of the variable domain of an Ig superfamily molecule, which method comprises:

(a) providing a sample of double stranded (ds) nucleic acid which contains the target sequence;

- (b) denaturing the sample so as to separate the two strands;
- (c) annealing to the sample a forward and a back oligonucleotide primer, the forward primer being specific for a sequence at or adjacent the 3' end of the sense strand of the target sequence, the back primer being specific for a sequence at or adjacent the 3' end of the antisense strand of the target sequence, under conditions which allow the primers to hybridise to the nucleic acid at or adjacent the target sequence;
- 5 (d) treating the annealed sample with a DNA polymerase enzyme in the presence of deoxynucleoside triphosphates under conditions which cause primer extension to take place; and
- (e) denaturing the sample under conditions such that the extended primers become separated from the target sequence.

10 Preferably, the method of the present invention further includes the step (f) of repeating steps (c) to (e) on the denatured mixture a plurality of times.

Preferably, the method of the present invention is used to clone complete variable domains from Ig molecules, most preferably from Ig heavy chains.

15 In step (c) recited above, the forward primer becomes annealed to the sense strand of the target sequence at or adjacent the 3' end of the strand. In a similar manner, the back primer becomes annealed to the antisense strand of the target sequence at or adjacent the 3' end of the strand. Thus, the forward primer anneals at or adjacent the region of the ds nucleic acid which encodes the C terminal end of the variable region or domain. Similarly, the back primer anneals at or adjacent the region of the ds nucleic acid which 20 encodes the N-terminal end of the variable domain.

In step (d), nucleotides are added onto the 3' end of the forward and back primers in accordance with the sequence of the strand to which they are annealed. Primer extension will continue in this manner until stopped by the beginning of the denaturing step (e). It must therefore be ensured that step (d) is carried out for a long enough time to ensure that the primers are extended so that the extended strands totally overlap 25 one another.

In step (e), the extended primers are separated from the ds nucleic acid. The ds nucleic acid can then serve again as a substrate to which further primers can anneal. Moreover, the extended primers themselves have the necessary complementary sequences to enable the primers to anneal thereto.

During further cycles, if step (f) is used, the amount of extended primers will increase exponentially so 30 that at the end of the cycles there will be a large quantity of cDNA having sequences complementary to the sense and antisense strands of the target sequence. Thus, the method of the present invention will result in the accumulation of a large quantity of cDNA which can form ds cDNA encoding at least part of the variable domain.

As will be apparent to the skilled person, some of the steps in the method may be carried out 35 simultaneously or sequentially as desired.

The forward and back primers may be provided as isolated oligonucleotides, in which case only two oligonucleotides will be used. However, alternatively the forward and back primers may each be supplied as a mixture of closely related oligonucleotides. For instance, it may be found that at a particular point in the sequence to which the primer is to anneal, there is the possibility of nucleotide variation. In this case a 40 primer may be used for each possible nucleotide variation. Furthermore it may be possible to use two or more sets of "nested" primers in the method to enhance the specific cloning of variable region genes.

The method described above is similar to the method described by Saiki et al. [17]. A similar method is also used in the methods described in EP-A-0 200 362. In both cases the method described is carried out using primers which are known to anneal efficiently to the specified nucleotide sequence. In neither of these 45 disclosures was it suggested that the method could be used to clone Ig parts of variable domain encoding sequences, where the target sequence contains inherently highly variable areas.

The ds nucleic acid sequence used in the method of the present invention may be derived from mRNA. For instance, RNA may be isolated in known manner from a cell or cell line which is known to produce IgS. mRNA may be separated from other RNA by oligo-dT chromatography. A complementary strand of cDNA 50 may then be synthesised on the mRNA template, using reverse transcriptase and a suitable primer, to yield an RNA/DNA heteroduplex. A second strand of DNA can be made in one of several ways, for example, by priming with RNA fragments of the mRNA strand (made by incubating RNA/DNA heteroduplex with RNase H) and using DNA polymerase, or by priming with a synthetic oligodeoxynucleotide primer which anneals to the 3' end of the first strand and using DNA polymerase. It has been found that the method of the present 55 invention can be carried out using ds cDNA prepared in this way.

When making such ds cDNA, it is possible to use a forward primer which anneals to a sequence in the CH1 domain (for a heavy chain variable domain) or the C λ or C μ domain (for a light chain variable domain). These will be located in close enough proximity to the target sequence to allow the sequence to be cloned.

The back primer may be one which anneals to a sequence at the N-terminal end of the VH1, V_x or V_λ domain. The back primer may consist of a plurality of primers having a variety of sequences designed to be complementary to the various families of VH1, V_x or V_λ sequences known. Alternatively the back primer may be a single primer having a consensus sequence derived from all the families of variable region genes.

Surprisingly, it has been found that the method of the present invention can be carried out using genomic DNA. If genomic DNA is used, there is a very large amount of DNA present, including actual coding sequences, introns and untranslated sequences between genes. Thus, there is considerable scope for non-specific annealing under the conditions used. However, it has surprisingly been found that there is very little non-specific annealing. It is therefore unexpected that it has proved possible to clone the genes of Ig-variable domains from genomic DNA.

Under some circumstances the use of genomic DNA may prove advantageous compared with use of mRNA, as the mRNA is readily degraded, and especially difficult to prepare from clinical samples of human tissue.

Thus, in accordance with an aspect of the present invention, the ds nucleic acid used in step (a) is genomic DNA.

When using genomic DNA as the ds nucleic acid source, it will not be possible to use as the forward primer an oligonucleotide having a sequence complementary to a sequence in a constant domain. This is because, in genomic DNA, the constant domain genes are generally separated from the variable domain genes by a considerable number of base pairs. Thus, the site of annealing would be too remote from the sequence to be cloned.

It should be noted that the method of the present invention can be used to clone both rearranged and unrearranged variable domain sequences from genomic DNA. It is known that in germ line genomic DNA the three genes, encoding the VH, DH and JH respectively, are separated from one another by considerable numbers of base pairs. On maturation of the immune response, these genes are rearranged so that the VH, DH and JH genes are fused together to provide the gene encoding the whole variable domain (see Figure 1). By using a forward primer specific for a sequence at or adjacent the 3' end of the sense strand of the genomic "unrearranged" VH gene, it is possible to clone the "unrearranged" VH gene alone, without also cloning the DH and JH genes. This can be of use in that it will then be possible to fuse the VH gene onto pre-cloned or synthetic DH and DH genes. In this way, rearrangement of the variable domain genes can be carried out *in vitro*.

The oligonucleotide primers used in step (c) may be specifically designed for use with a particular target sequence. In this case, it will be necessary to sequence at least the 5' and 3' ends of the target sequence so that the appropriate oligonucleotides can be synthesised. However, the present inventors have discovered that it is not necessary to use such specifically designed primers. Instead, it is possible to use a species specific general primer or a mixture of such primers for annealing to each end of the target sequence. This is not particularly surprising as regards the 3' end of the target sequence. It is known that this end of the variable domain encoding sequence leads into a segment encoding JH which is known to be relatively conserved. However, it was surprisingly discovered that, within a single species, the sequence at the 5' end of the target sequence is sufficiently well conserved to enable a species specific general primer or a mixture thereof to be designed for the 5' end of the target sequence.

Therefore according to a preferred aspect of the present invention, in step (c) the two primers which are used are species specific general primers, whether used as single primers or as mixtures of primers. This greatly facilitates the cloning of any undetermined target sequence since it will avoid the need to carry out any sequencing on the target sequence in order to produce target sequence-specific primers. Thus the method of this aspect of the invention provides a general method for cloning variable region or domain encoding sequences of a particular species.

Once the variable domain gene has been cloned using the method described above, it may be directly inserted into an expression vector, for instance using the PCR reaction to paste the gene into a vector.

Advantageously, however, each primer includes a sequence including a restriction enzyme recognition site. The sequence recognised by the restriction enzyme need not be in the part of the primer which anneals to the ds nucleic acid, but may be provided as an extension which does not anneal. The use of primers with restriction sites has the advantage that the DNA can be cut with at least one restriction enzyme which leaves 3' or 5' overhanging nucleotides. Such DNA is more readily cloned into the corresponding sites on the vectors than blunt end fragments taken directly from the method. The ds cDNA produced at the end of the cycles will thus be readily insertable into a cloning vector by use of the appropriate restriction enzymes. Preferably the choice of restriction sites is such that the ds cDNA is cloned directly into an expression vector, such that the ligand encoded by the gene is expressed. In this case the restriction site is preferably located in the sequence which is annealed to the ds nucleic acid.

Since the primers may not have a sequence exactly complementary to the target sequence to which it is to be annealed, for instance because of nucleotide variations or because of the introduction of a restriction enzyme recognition site, it may be necessary to adjust the conditions in the annealing mixture to enable the primers to anneal to the ds nucleic acid. This is well within the competence of the person skilled in the art and needs no further explanation.

In step (d), any DNA polymerase may be used. Such polymerases are known in the art and are available commercially. The conditions to be used with each polymerase are well known and require no further explanation here. The polymerase reaction will need to be carried out in the presence of the four nucleoside triphosphates. These and the polymerase enzyme may already be present in the sample or may be provided afresh for each cycle.

The denaturing step (e) may be carried out, for instance, by heating the sample, by use of chaotropic agents, such as urea or guanidine, or by the use of changes in ionic strength or pH. Preferably, denaturing is carried out by heating since this is readily reversible. Where heating is used to carry out the denaturing, it will be usual to use a thermostable DNA polymerase, such as Taq polymerase, since this will not need replenishing at each cycle.

If heating is used to control the method, a suitable cycle of heating comprises denaturation at about 95 °C for about 1 minute, annealing at from 30 °C to 65 °C for about 1 minute and primer extension at about 75 °C for about 2 minutes. To ensure that elongation and renaturation is complete, the mixture after the final cycle is preferably held at about 60 °C for about 5 minutes.

The product ds cDNA may be separated from the mixture for instance by gel electrophoresis using agarose gels. However, if desired, the ds cDNA may be used in unpurified form and inserted directly into a suitable cloning or expression vector by conventional methods. This will be particularly easy to accomplish if the primers include restriction enzyme recognition sequences.

The method of the present invention may be used to make variations in the sequences encoding the variable domains. For example this may be achieved by using a mixture of related oligonucleotide primers as at least one of the primers. Preferably the primers are particularly variable in the middle of the primer and relatively conserved at the 5' and 3' ends. Preferably the ends of the primers are complementary to the framework regions of the variable domain, and the variable region in the middle of the primer covers all or part of a CDR. Preferably a forward primer is used in the area which forms the third CDR. If the method is carried out using such a mixture of oligonucleotides, the product will be a mixture of variable domain encoding sequences. Moreover, variations in the sequence may be introduced by incorporating some mutagenic nucleotide triphosphates in step (d), such that point mutations are scattered throughout the target region. Alternatively such point mutations are introduced by performing a large number of cycles of amplification, as errors due to the natural error rate of the DNA polymerase are amplified, particularly when using high concentrations of nucleoside triphosphates.

The method of this aspect of the present invention has the advantage that it greatly facilitates the cloning of variable domain encoding sequences directly from mRNA or genomic DNA. This in turn will facilitate the production of modified Ig-type molecules by any of the prior art methods referred to above. Further, target genes can be cloned from tissue samples containing antibody producing cells, and the genes can be sequenced. By doing this, it will be possible to look directly at the immune repertoire of a patient. This "fingerprinting" of a patient's immune repertoire could be of use in diagnosis, for instance of auto-immune diseases.

In step (a) the ds cDNA is derived from mRNA. For Ig derived variable domains, the mRNA is preferably be isolated from lymphocytes which have been stimulated to enhance production of mRNA.

In each step (c) the set of primers are preferably different from the previous step (c), so as to enhance the specificity of copying. Thus the sets of primers form a nested set. For example, for cloning of Ig heavy chain variable domains, the first set of primers may be located within the signal sequence and constant region, as described by Larrick et al., [18], and the second set of primers entirely within the variable region, as described by Orlandi et al., [19]. Preferably the primers of step (c) include restriction sites to facilitate subsequent cloning. In the last cycle the set of primers used in step (c) should preferably include restriction sites for introduction into expression vectors. Possible mismatches between the primers and the template strands may be corrected by "nick translation". ds cDNA is preferably cleaved with restriction enzymes at sites introduced into the primers to facilitate the cloning.

According to another aspect of the present invention the product ds cDNA is cloned directly into an expression vector. The host may be prokaryotic or eukaryotic, but is preferably bacterial. Preferably the choice of restriction sites in the primers and in the vector, and other features of the vector will allow the expression of complete ligands, while preserving all those features of the amino acid sequence which are typical of the (methoded) ligands. For example, for expression of the rearranged variable genes, the primers

would be chosen to allow the cloning of target sequences including at least all the three CDR sequences. The cloning vector would then encode a signal sequence (for secretion of the ligand), and sequences encoding the N-terminal end of the first framework region, restriction sites for cloning and then the C-terminal end of the last (fourth) framework region.

5 For expression of unrearranged VH genes as part of complete ligands, the primers would be chosen to allow the cloning of target sequences including at least the first two CDRs. The cloning vector could then encode signal sequence, the N-terminal end of the first framework region, restriction sites for cloning and then the C-terminal end of the third framework region, the third CDR and fourth framework region.

10 Primers and cloning vectors may likewise be devised for expression of single CDRs, particularly the third CDR, as parts of complete ligands. The advantage of cloning repertoires of single CDRs would permit the design of a "universal" set of framework regions, incorporating desirable properties such as solubility.

15 Single ligands could be expressed alone or in combination with a complementary variable domain. For example, a heavy chain variable domain can be expressed either as an individual domain or, if it is expressed with a complementary light chain variable domain, as an antigen binding site. Preferably the two partners would be expressed in the same cell, or secreted from the same cell, and the proteins allowed to associate non-covalently to form an Fv fragment. Thus the two genes encoding the complementary partners can be placed in tandem and expressed from a single vector, the vector including two sets of restriction sites.

20 Preferably the genes are introduced sequentially: for example the heavy chain variable domain can be cloned first and then the light chain variable domain. Alternatively the two genes are introduced into the vector in a single step, for example by using the polymerase chain reaction to paste together each gene with any necessary intervening sequence, as essentially described by Yon and Fried [29]. The two partners could be also expressed as a linked protein to produce a single chain Fv fragment, using similar vectors to those described above. As a further alternative the two genes may be placed in two different vectors, for example in which one vector is a phage vector and the other is a plasmid vector.

25 Moreover, the cloned ds cDNA may be inserted into an expression vector already containing sequences encoding one or more constant domains to allow the vector to express Ig-type chains. The expression of Fab fragments, for example, would have the advantage over Fv fragments that the heavy and light chains would tend to associate through the constant domains in addition to the variable domains. The final expression product may be any of the modified Ig-type molecules referred to above.

30 The cloned sequence may also be inserted into an expression vector so that it can be expressed as a fusion protein. The variable domain encoding sequence may be linked directly or via a linker sequence to a DNA sequence encoding any protein effector molecule, such as a toxin, enzyme, label or another ligand. The variable domain sequences may also be linked to proteins on the outer side of bacteria or phage. Thus, 35 the method of this aspect of the invention may be used to produce receptors according to the invention.

According to another aspect of the invention, the cloning of ds cDNA directly for expression permits the rapid construction of expression libraries which can be screened for binding activities. For Ig heavy and light chain variable genes, the ds cDNA may comprise variable genes isolated as complete rearranged genes from the animal, or variable genes built from several different sources, for example a repertoire of unrearranged VH genes combined with a synthetic repertoire of DH and JH genes. Preferably repertoires of genes encoding Ig heavy chain variable domains are prepared from lymphocytes of animals immunised with an antigen.

40 The screening method may take a range of formats well known in the art. For example Ig heavy chain variable domains secreted from bacteria may be screened by binding to antigen on a solid phase, and detecting the captured domains by antibodies. Thus the domains may be screened by growing the bacteria in liquid culture and binding to antigen coated on the surface of ELISA plates. However, preferably bacterial colonies (or phage plaques) which secrete ligands (or modified ligands, or ligand fusions with proteins) are screened for antigen binding on membranes. Either the ligands are bound directly to the membranes (and for example detected with labelled antigen), or captured on antigen coated membranes (and detected with reagents specific for ligands). The use of membranes offers great convenience in screening many clones, 45 and such techniques are well known in the art.

The screening method may also be greatly facilitated by making protein fusions with the ligands, for example by introducing a peptide tag which is recognised by an antibody at the N-terminal or C-terminal end of the ligand, or joining the ligand to an enzyme which catalyses the conversion of a colourless substrate to a coloured product. In the latter case, the binding of antigen may be detected simply by adding substrate. Alternatively, for ligands expressed and folded correctly inside eukaryotic cells, joining of the ligand and a domain of a transcriptional activator such as the GAL4 protein of yeast, and joining of antigen to the other domain of the GAL4 protein, could form the basis for screening binding activities, as described 50

by Fields and Song [21].

The preparation of proteins, or even cells with multiple copies of the ligands, may improve the avidity of the ligand for immobilised antigen, and hence the sensitivity of the screening method. For example, the ligand may be joined to a protein subunit of a multimeric protein, to a phage coat protein or to an outer membrane protein of *E. coli* such as ompA or lamB. Such fusions to phage or bacterial proteins also offers possibilities of selecting bacteria displaying ligands with antigen binding activities. For example such bacteria may be precipitated with antigen bound to a solid support, or may be subjected to affinity chromatography, or may be bound to larger cells or particles which have been coated with antigen and sorted using a fluorescence activated cell sorter (FACS). The proteins or peptides fused to the ligands are preferably encoded by the vector, such that cloning of the ds cDNA repertoire creates the fusion product.

In addition to screening for binding activities of single ligands, it may be necessary to screen for binding or catalytic activities of associated ligands, for example, the associated Ig heavy and light chain variable domains. For example, repertoires of heavy and light chain variable genes may be cloned such that two domains are expressed together. Only some of the pairs of domains may associate, and only some of these associated pairs may bind to antigen. The repertoires of heavy and light chain variable domains could be cloned such that each domain is paired at random. This approach may be most suitable for isolation of associated domains in which the presence of both partners is required to form a cleft. Alternatively, to allow the binding of hapten. Alternatively, since the repertoires of light chain sequences are less diverse than those of heavy chains, a small repertoire of light chain variable domains, for example including representative members of each family of domains, may be combined with a large repertoire of heavy chain variable domains.

Preferably however, a repertoire of heavy chain variable domains is screened first for antigen binding in the absence of the light chain partner, and then only those heavy chain variable domains binding to antigen are combined with the repertoire of light chain variable domains. Binding of associated heavy and light chain variable domains may be distinguished readily from binding of single domains, for example by fusing each domain to a different C-terminal peptide tag which are specifically recognised by different monoclonal antibodies.

The hierarchical approach of first cloning heavy chain variable domains with binding activities, then cloning matching light chain variable domains may be particularly appropriate for the construction of catalytic antibodies, as the heavy chain may be screened first for substrate binding. A light chain variable domain would then be identified which is capable of association with the heavy chain, and "catalytic" residues such as cysteine or histidine (or prosthetic groups) would be introduced into the CDRs to stabilise the transition state or attack the substrate, as described by Baldwin and Schultz [22].

Although the binding activities of non-covalently associated heavy and light chain variable domains (Fv fragments) may be screened, suitable fusion proteins may drive the association of the variable domain partners. Thus Fab fragments are more likely to be associated than the Fv fragments, as the heavy chain variable domain is attached to a single heavy chain constant domain, and the light chain variable domain is attached to a single light chain variable domain, and the two constant domains associate together.

Alternatively the heavy and light chain variable domains are covalently linked together with a peptide, as in the single chain antibodies, or peptide sequences attached, preferably at the C-terminal end which will associate through forming cysteine bonds or through non-covalent interactions, such as the introduction of "leucine zipper" motifs. However, in order to isolate pairs of tightly associated variable domains, the Fv fragments are preferably used.

The construction of Fv fragments isolated from a repertoire of variable region genes offers a way of building complete antibodies, and an alternative to hybridoma technology. For example by attaching the variable domains to light or suitable heavy chain constant domains, as appropriate, and expressing the assembled genes in mammalian cells, complete antibodies may be made and should possess natural effector functions, such as complement lysis. This route is particularly attractive for the construction of human monoclonal antibodies, as hybridoma technology has proved difficult, and for example, although human peripheral blood lymphocytes can be immortalised with Epstein Barr virus, such hybridomas tend to secrete low affinity IgM antibodies.

Moreover, it is known that immunological mechanisms ensure that lymphocytes do not generally secrete antibodies directed against host proteins. However it is desirable to make human antibodies directed against human proteins, for example to human cell surface markers to treat cancers, or to histocompatibility antigens to treat auto-immune diseases. The construction of human antibodies built from the combinatorial repertoire of heavy and light chain variable domains may overcome this problem, as it will allow human antibodies to be built with specificities which would normally have been eliminated.

The method also offers a new way of making bispecific antibodies. Antibodies with dual specificity can be made by fusing two hybridomas of different specificities, so as to make a hybrid antibody with an Fab arm of one specificity, and the other Fab arm of a second specificity. However the yields of the bispecific antibody are low, as heavy and light chains also find the wrong partners. The construction of Fv fragments which are tightly associated should preferentially drive the association of the correct pairs of heavy with light chains. (It would not assist in the correct pairing of the two heavy chains with each other.) The improved production of bispecific antibodies would have a variety of applications in diagnosis and therapy, as is well known.

Thus the invention provides a species specific general oligonucleotide primer or a mixture of such primers useful for cloning variable domain encoding sequences from animals of that species. The method allows a single pair or pair of mixtures of species specific general primers to be used to clone any desired antibody specificity from that species. This eliminates the need to carry out any sequencing of the target sequence to be cloned and the need to design specific primers for each specificity to be recovered.

Furthermore it provides for the construction of repertoires of variable genes, for the expression of the variable genes directly on cloning, for the screening of the encoded domains for binding activities and for the assembly of the domains with other variable domains derived from the repertoire.

Thus the use of the method of the present invention will allow for the production of heavy chain variable domains with binding activities and variants of these domains. It allows for the production of monoclonal antibodies and bispecific antibodies, and will provide an alternative to hybridoma technology. For instance, mouse splenic ds mRNA or genomic DNA may be obtained from a hyperimmunised mouse. This could be cloned using the method of the present invention and then the cloned ds DNA inserted into a suitable expression vector. The expression vector would be used to transform a host cell, for instance a bacterial cell, to enable it to produce an Fv fragment or a Fab fragment. The Fv or Fab fragment would then be built into a monoclonal antibody by attaching constant domains and expressing it in mammalian cells.

The present invention is now described, by way of example only, with reference to the accompanying drawings in which:

Figure 1 shows a schematic representation of the unrearranged and rearranged heavy and light chain variable genes and the location of the primers;
 Figure 2 shows a schematic representation of the M13-VHPCR1 vector and a cloning scheme for amplified heavy chain variable domains;
 Figure 3 shows the sequence of the Ig variable region derived sequences in M13-VHPCR1;
 Figure 4 shows a schematic representation of the M13-VKPCR1 vector and a cloning scheme for light chain variable domains;
 Figure 5 shows the sequence of the Ig variable region derived sequences in M13-VKPCR1;
 Figure 6 shows the nucleotide sequences of the heavy and light chain variable domain encoding sequences of MAb MBr1;
 Figure 7 shows a schematic representation of the pSV-gpt vector (also known as α -Lys 30) which contains a variable region cloned as a HindIII-BamHI fragment, which is excised on introducing the new variable region. The gene for human IgG1 has also been engineered to remove a BamHI site, such that the BamHI site in the vector is unique;
 Figure 8 shows a schematic representation of the pSV-hydro vector (also known as α -Lys 17). It is derived from pSV gpt vector with the gene encoding mycophenolic acid replaced by a gene coding for hygromycin resistance. The construct contains a variable gene cloned as a HindIII-BamHI fragment which is excised on introducing the new variable region. The gene for human Cx has also been engineered to remove a BamHI site, such that the BamHI site in the vector is unique;
 Figure 9 shows the assembly of the mouse: human MBr1 chimaeric antibody;
 Figure 10 shows encoded amino acid sequences of 48 mouse rearranged VH genes;
 Figure 11 shows encoded amino acid sequences of human rearranged VH genes;
 Figure 12 shows encoded amino acid sequences of unrearranged human VH genes;
 Figure 13 shows the sequence of part of the plasmid pSW1: essentially the sequence of a pectate lyase leader linked to VHLYS in pSW1 and cloned as an SphI-EcoRI fragment into pUC19 and the translation of the open reading frame encoding the pectate lyase leader-VHLYS polypeptide being shown;
 Figure 14 shows the sequence of part of the plasmid pSW2: essentially the sequence of a pectate lyase leader linked to VHLYS and to VKLYS, and cloned as an SphI-EcoRI-EcoRI fragment into pUC19 and the translation of open reading frames encoding the pectate lyase leader-VHLYS and pectate lyase leader-VKLYS polypeptides being shown;
 Figure 15 shows the sequence of part of the plasmid pSW1HPOLYMYC which is based on pSW1 and in which a polylinker sequence has replaced the variable domain of VHLYS, and acts as a cloning site for

amplified VH genes, and a peptide tag is introduced at the C-terminal end; Figure 16 shows the encoded amino acid sequences of two VH domains derived from mouse spleen and having lysozyme binding activity, and compared with the VH domain of the D1,3 antibody. The arrows mark the points of difference between the two VH domains;

- 5 Figure 17 shows the encoded amino acid sequence of a VH domain derived from human peripheral blood lymphocytes and having lysozyme binding activity;
- Figure 18 shows a scheme for generating and cloning mutants of the VHLYS gene, which is compared with the scheme for cloning natural repertoires of VH genes;
- Figure 19 shows the sequence of part of the vector pSW2HPOLY;
- 10 Figure 20 shows the sequence of part of the vector pSW3 which encodes the two linked VHLYS domains;
- Figure 21 shows the sequence of the VHLYS domain and pElB leader sequence fused to the alkaline phosphatase gene;
- 15 Figure 22 shows the sequence of the vector pSW1VHLYSVKPOLYMYC for expression of a repertoire of V_x light chain variable domains in association with the VHLYS domain; and
- Figure 23 shows the sequence of VH domain which is secreted at high levels from *E. coli*. The differences with VHLYS domain are marked.

PRIMERS

- 20 In the Examples described below, the following oligonucleotide primers, or mixed primers were used. Their locations are marked on Figure 1 and sequences are as follows:

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VH1FOR 5' TGAGGAGACGGTGACCGTGGTCCCTTGGCCCCAG 3';
 VH1FOR-2 5' TGAGGAGACGGTGACCGTGGTCCCTTGGCCCC 3';

5 Hu1VHFOR 5' CTTGGTGGAGGCTGAGGAGACGGTGACC 3';
 Hu2VHFOR 5' CTTGGTGGAGGCTGAGGAGACGGTGACC 3';
 10 Hu3VHFOR 5' CTTGGTGGATGCTGAGGAGACGGTGACC 3';
 Hu4VHFOR 5' CTTGGTGGATGCTGAGGAGACGGTGACC 3';

MOJH1FOR 5' TGAGGAGACGGTGACCGTGGTCCCTGCGCCCCAG 3';
 15 MOJH2FOR 5' TGAGGAGACGGTGACCGTGGTGCCTTGGCCCCAG 3';
 MOJH3FOR 5' TGCAGAGACGGTGACCAGAGTCCCTTGGCCCCAG 3';
 MOJH4FOR 5' TGAGGAGACGGTGACCGAGGTTCCCTTGACCCCAG 3';

20 HUJH1FOR 5' TGAGGAGACGGTGACCAGGGTGCCTTGGCCCCAG 3';
 HUJH2FOR 5' TGAGGAGACGGTGACCAGGGTGCCACGGCCCCAG 3';
 25 HUJH4FOR 5' TGAGGAGACGGTGACCAGGGTTCCCTTGGCCCCAG 3';

VK1FOR 5' GTTAGATCTCCAGCTTGGTCCC 3';
 VK2FOR 5' CGTTAGATCTCCAGCTTGGTCCC 3';
 30 VK3FOR 5' CCGTTTCAGCTCGAGCTTGGTCCC 3';

MOJK1FOR 5' CGTTAGATCTCCAGCTTGGTGCC 3';
 35 MOJK3FOR 5' GGTTAGATCTCCAGTCTGGTCCC 3';
 MOJK4FOR 5' CGTTAGATCTCCAACTTGTCCC 3';

40 HUJK1FOR 5' CGTTAGATCTCACCTTGGTCCC 3';
 HUJK3FOR 5' CGTTAGATCTCCACTTGGTCCC 3';
 HUJK4FOR 5' CGTTAGATCTCACCTTGGTCCC 3';
 45 HUJK5FOR 5' CGTTAGATCTCCAGTCGTGTCCC 3';

VH1BACK 5' AGGT(C/G)(C/A)A(G/A)CTGCAG(G/C)AGTC(T/A)GG 3';

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5	Hu2VHIBACK:	5' CAGGTGCAGCTGCAGCAGTCTGG 3';
	HuVHIIBACK:	5' CAGGTGCAGCTGCAGGAGTCGGG 3';
	Hu2VHIIIBACK:	5' GAGGTGCAGCTGCAGGAGTCTGG 3';
	HuVHIVBACK:	5' CAGGTGCAGCTGCAGCAGTCTGG 3';
10	MOVHIBACK	5' AGGTGCAGCTGCAGGAGTCAG 3';
	MOVHIIABACK	5' AGGTCCAGCTGCAGCA(G/A)TCTGG 3';
	MOVHIIIBACK	5' AGGTCCAAGTCAGCAGCAGCCTGG 3';
	MOVHIIIBACK	5' AGGTGAAGCTGCAGGAGTCTGG 3';
15		
	VK1BACK	5' GACATTCAAGCTGACCCAGTCTCCA 3';
	VK2BACK	5' GACATTGAGCTCACCCAGTCTCCA 3';
20		
	MOVKIIABACK	5' GATGTTCAAGCTGACCCAAACTCCA 3'
	MOVKIIIBACK	5' GATATTCAAGCTGACCCAGGATGAA 3';
25		
	HuHep1FOR	5' C(A/G)(C/G)TGAGCTCACTGTGTCTCTCGCACA 3';
	HuOcta1BACK	5' CGTGAATATGCAAATAA 3';
	HuOcta2BACK	5' AGTAGGAGACATGCAAAT 3'; and
30		
	HuOcta3BACK	5' CACCACCCACATGCAAAT 3';
35		
	VHMUT1	5' GGAGACGGTGACCGTGGTCCCTTGGCCCCAGTAGTCAAG NNNNNNNNNNNNCTCTCTGGC 3' (where N is an equimolar mixture of T, C, G and A)
	M13 pRIMER	5' AACAGCTATGACCATG 3' (New England Biolabs *1201)
40		

EXAMPLE 1

45 Cloning of Mouse Rearranged Variable region genes from hybridomas, assembly of genes encoding chimaeric antibodies and the expression of antibodies from myeloma cells

VH1FOR is designed to anneal with the 3' end of the sense strand of any mouse heavy chain variable domain encoding sequence. It contains a BstEII recognition site. VK1FOR is designed to anneal with the 3' end of the sense strand of any mouse kappa-type light chain variable domain encoding sequence and contains a BgIII recognition site. VH1BACK is designed to anneal with the 3' end of the antisense strand of any mouse heavy chain variable domain and contains a PstI recognition site. VK1BACK is designed to anneal with the 3' end of the antisense strand of any mouse kappa-type light chain variable domain encoding sequence and contains a Pvull recognition site.

In this Example five mouse hybridomas were used as a source of ds nucleic acid. The hybridomas produce monoclonal antibodies (MAbs) designated MBr1 [23], BW431/26 [24], BW494/32 [25], BW250/183 [24,26] and BW704/152 [27]. MAb MBr1 is particularly interesting in that it is known to be specific for a

saccharide epitope on a human mammary carcinoma line MCF-7 [28].

Cloning via mRNA

5 Each of the five hybridomas referred to above was grown up in roller bottles and about 5×10^8 cells of each hybridoma were used to isolate RNA. mRNA was separated from the isolated RNA using oligodT cellulose [29]. First strand cDNA was synthesised according to the procedure described by Maniatis et al. [30] as set out below.

10 In order to clone the heavy chain variable domain encoding sequence, a 50 μl reaction solution which contains 10 μg mRNA, 20 pmole VH1FOR primer, 250 μM each of dATP, dTTP, dCTP and dGTP, 10 mM dithiothreitol (DTT), 100 mM Tris.HCl, 10 mM MgCl₂ and 140 mM KCl, adjusted to pH 8.3 was prepared. The reaction solution was heated at 70 °C for ten minutes and allowed to cool to anneal the primer to the 3' end of the variable domain encoding sequence in the mRNA. To the reaction solution was then added 46 units of reverse transcriptase (Anglian Biotec) and the solution was then incubated at 42 °C for 1 hour to cause first strand cDNA synthesis.

15 In order to clone the light chain variable domain encoding sequence, the same procedure as set out above was used except that the VK1FOR primer was used in place of the VH1FOR primer.

Amplification from RNA/DNA hybrid

20 Once the ds RNA/DNA hybrids had been produced, the variable domain encoding sequences were amplified as follows. For heavy chain variable domain encoding sequence amplification, a 50 μl reaction solution containing 5 μl of the ds RNA/DNA hybrid-containing solution, 25 pmole each of VH1FOR and VH1BACK primers, 250 μM of dATP, dTTP, dCTP and dGTP, 67 mM Tris.HCl, 17 mM ammonium sulphate, 10 mM MgCl₂, 200 $\mu\text{g}/\text{ml}$ gelatine and 2 units Taq polymerase (Cetus) was prepared. The reaction solution was overlaid with paraffin oil and subjected to 25 rounds of temperature cycling using a Techne PHC-1 programmable heating block. Each cycle consisted of 1 minute and 95 °C (to denature the nucleic acids), 1 minute at 30 °C (to anneal the primers to the nucleic acids) and 2 minutes at 72 °C (to cause elongation from the primers). After the 25 cycles, the reaction solution and the oil were extracted twice with ether, once with phenol and once with phenol/CHCl₃. Thereafter ds cDNA was precipitated with ethanol. The precipitated ds cDNA was then taken up in 50 μl of water and frozen.

The procedure for light chain amplification was exactly as described above, except that the VK1FOR and VK1BACK primers were used in place of the VH1FOR and VH1BACK primers respectively.

35 5 μl of each sample of amplified cDNA was fractionated on 2% agarose gels by electrophoresis and stained with ethidium bromide. This showed that the amplified ds cDNA gave a major band of the expected size (about 330 bp). (However the band for VK DNA of MBr1 was very weak. It was therefore excised from the gel and reamplified in a second round.) Thus by this simple procedure, reasonable quantities of ds DNA encoding the light and heavy chain variable domains of the five MAbs were produced.

40 Heavy Chain Vector Construction

A BstEII recognition site was introduced into the vector M13-HuVHNP [31] by site directed mutagenesis [32,33] to produce the vector M13-VHPCR1 (Figures 2 and 3).

45 Each amplified heavy chain variable domain encoding sequence was digested with the restriction enzymes PstI and BstEII. The fragments were phenol extracted, purified on 2% low melting point agarose gels and force cloned into vector M13-VHPCR1 which had been digested with PstI and BstEII and purified on an 0.8% agarose gel. Clones containing the variable domain inserts were identified directly by sequencing [34] using primers based in the 3' non-coding variable gene in the M13-VHPCR1 vector.

50 There is an internal PstI site in the heavy chain variable domain encoding sequences of BW431/26. This variable domain encoding sequence was therefore assembled in two steps. The 3' PstI-BstEII fragment was first cloned into M13-VHPCR1, followed in a second step by the 5' PstI fragment.

Light Chain Vector Construction

55 Vector M13mp18 [35] was cut with Pvull and the vector backbone was blunt ligated to a synthetic HindIII-BamHI polylinker. Vector M13-HuVKLYS [36] was digested with HindIII and BamHI to isolate the HuVKLYS gene. This HindIII-BamHI fragment was then inserted into the HindIII-BamHI polylinker site to form a vector M13-VKPCR1 which lacks any Pvull sites in the vector backbone (Figures 4 and 5). This

vector was prepared in E Coli JM110 [22] to avoid dam methylation at the BclI site.

Each amplified light chain variable domain encoding sequence was digested with Pvull and BgIII. The fragments were phenol extracted, purified on 2% low melting point agarose gels and force cloned into vector M13-VKPCR1 which had been digested with Pvull and BclI, purified on an 0.8% agarose gel and

- 5 treated with calf intestinal phosphatase. Clones containing the light chain variable region inserts were identified directly by sequencing [34] using primers based in the 3' non-coding region of the variable domain in the M13-VKPCR1 vector.

The nucleotide sequences of the MBr1 heavy and light chain variable domains are shown in Figure 6 with part of the flanking regions of the M13-VHPCR1 and M13-VKPCR1 vectors.

10

Antibody Expression

The HindIII-BamHI fragment carrying the MBr1 heavy chain variable domain encoding sequence in M13-VHPCR1 was recloned into a pSV-gpt vector with human γ 1 constant regions [37] (Figure 7). The MBr1 light chain variable domain encoding sequence in M13-VKPCR1 was recloned as a HindIII-BamHI fragment into a pSV vector, PSV-hyg-HuCK with a hygromycin resistance marker and a human kappa constant domain (Figure 8). The assembly of the genes is summarised in Figure 9.

The vectors thus produced were linearised with Pvul (in the case of the pSV-hydro vectors the Pvul digest is only partial) and cotransfected into the non-secreting mouse myeloma line NSO [38] by 20 electroporation [39]. One day after cotransfection, cells were selected in 0.3 μ g/ml mycophenolic acid (MPA) and after seven days in 1 μ g/ml MPA. After 14 days, four wells, each containing one or two major colonies, were screened by incorporation of 14 C-lysine [40] and the secreted antibody detected after precipitation with protein-A Sepharose™ (Pharmacia) on SDS-PAGE [41]. The gels were stained, fixed, soaked in a fluorographic reagent, Amplify™ (Amersham), dried and autoradiographed on preflashed film at 25 -70 °C for 2 days.

Supernatant was also tested for binding to the mammary carcinoma line MCF-7 and the colon carcinoma line HT-29, essentially as described by Menard et al. [23], either by an indirect immunofluorescence assay on cell suspensions (using a fluorescein-labelled goat anti-human IgG (Amersham)) or by a solid phase RIA on monolayers of fixed cells (using 125 I-protein A (Amersham)).

30 It was found that one of the supernatants from the four wells contained secreted antibody. The chimeric antibody in the supernatant, like the parent mouse MBr1 antibody, was found to bind to MCF-7 cells but not the HT-29 cells, thus showing that the specificity had been properly cloned and expressed.

Example 2

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Cloning of rearranged variable genes from genomic DNA of mouse spleen

Preparation of DNA from spleen.

40 The DNA from the mouse spleen was prepared in one of two ways (although other ways can be used).

Method 1. A mouse spleen was cut into two pieces and each piece was put into a standard Eppendorf tube with 200 μ l of PBS. The tip of a 1 ml glass pipette was closed and rounded in the blue flame of a Bunsen burner. The pipette was used to squash the spleen piece in each tube. The cells thus produced were transferred to a fresh Eppendorf tube and the method was repeated three times until the connective 45 tissue of the spleen appeared white. Any connective tissue which has been transferred with the cells was removed using a drawn-out Pasteur pipette. The cells were then washed in PBS and distributed into four tubes.

The mouse spleen cells were then sedimented by a 2 minute spin in a Microcentaur centrifuge at low speed setting. All the supernatant was aspirated with a drawn out Pasteur pipette. If desired, at this point 50 the cell sample can be frozen and stored at -20 °C

To the cell sample (once thawed if it had been frozen) was added 500 μ l of water and 5 μ l of a 10% solution of NP-40, a non-ionic detergent. The tube was closed and a hole was punched in the lid. The tube was placed on a boiling water bath for 5 minutes to disrupt the cells and was then cooled on ice for 5 minutes. The tube was then spun for 2 minutes at high speed to remove cell debris.

55 The supernatant was transferred to a new tube and to this was added 125 μ l 5M NaCl and 30 μ l 1M MOPS adjusted to pH 7.0. The DNA in the supernatant was absorbed on a Quiagen 5 tip and purified following the manufacturer's instructions for lambda DNA. After isopropanol precipitation, the DNA was resuspended in 500 μ l water.

Method 2. This method is based on the technique described in Maniatis et al. [30]. A mouse spleen was cut into very fine pieces and put into a 2 ml glass homogeniser. The cells were then freed from the tissue by several slow up and down strokes with the piston. The cell suspension was made in 500 µl phosphate buffered saline (PBS) and transferred to an Eppendorf tube. The cells were then spun for 2 min at low speed in a Microcentaur centrifuge. This results in a visible separation of white and red cells. The white cells, sedimenting slower, form a layer on top of the red cells. The supernatant was carefully removed and spun to ensure that all the white cells had sedimented. The layer of white cells was resuspended in two portions of 500 µl PBS and transferred to another tube.

The white cells were precipitated by spinning in the Microcentaur centrifuge at low speed for one minute. The cells were washed a further two times with 500 µl PBS, and were finally resuspended in 200 µl PBS. The white cells were added to 2.5 ml 25 mM EDTA and 10 mM Tris.Cl, pH 7.4, and vortexed slowly. While vortexing 25 µl 20% SDS was added. The cells lysed immediately and the solution became viscous and clear. 100 µl of 20 mg/ml proteinase K was added and incubated one to three hours at 50 °C.

The sample was extracted with an equal volume of phenol and the same volume of chloroform, and vortexed. After centrifuging, the aqueous phase was removed and 1/10 volume 3M ammonium acetate was added. This was overlaid with three volumes of cold ethanol and the tube rocked carefully until the DNA strands became visible. The DNA was spooled out with a Pasteur pipette, the ethanol allowed to drip off, and the DNA transferred to 1 ml of 10 mM Tris.Cl pH 7.4, 0.1 mM EDTA in an Eppendorf tube. The DNA was allowed to dissolve in the cold overnight on a roller.

20

Amplification from genomic DNA.

The DNA solution was diluted 1/10 in water and boiled for 5 min prior to using the polymerase chain reaction (PCR). For each PCR reaction, typically 50-200 ng of DNA were used.

25 The heavy and light chain variable domain encoding sequences in the genomic DNA isolated from the human PBL or the mouse spleen cells was then amplified and cloned using the general protocol described in the first two paragraphs of the section headed "Amplification from RNA/DNA Hybrid" in Example 1, except that during the annealing part of each cycle, the temperature was held at 65 °C and that 30 cycles were used. Furthermore, to minimise the annealing between the 3' ends of the two primers, the sample was 30 first heated to 95 °C, then annealed at 65 °C, and only then was the Taq polymerase added. At the end of the 30 cycles, the reaction mixture was held at 60 °C for five minutes to ensure that complete elongation and renaturation of the amplified fragments had taken place.

The primers used to amplify the mouse spleen genomic DNA were VH1FOR and VH1BACK, for the heavy chain variable domain and VK2FOR and VK1BACK, for the light chain variable domain. (VK2FOR only differs from VK1FOR in that it has an extra C residue on the 5' end.)

40 Other sets of primers, designed to optimise annealing with different families of mouse VH and V_x genes were devised and used in mixtures with the primers above. For example, mixtures of VK1FOR, MOJK1FOR, MOJK3FOR and MOJK4FOR were used as forward primers and mixtures of VK1BACK, MOVKIIBACK and MOVKIBACK as back primers for amplification of V_x genes. Likewise mixtures of VH1FOR, MOJH1FOR, MOJH2FOR, MOJH3FOR and MOJH4FOR were used as forward primers and mixtures of VH1BACK, MOVHIBACK, MOVHIIBACK, MOVHIIIBACK, MOVHIIIBACK were used as backward primers for amplification of VH genes.

All these heavy chain FOR primers referred to above contain a BstEII site and all the BACK primers referred to above contain a PstI site. These light chain FOR and BACK primers referred to above all contain BgIII and Pvull sites respectively. Light chain primers (VK3FOR and VK2BACK) were also devised which utilised different restriction sites, SacI and Xhol.

45 Typically all these primers yielded amplified DNA of the correct size on gel electrophoresis, although other bands were also present. However, a problem was identified in which the 5' and 3' ends of the forward and backward primers for the VH genes were partially complementary, and this could yield a major band of "primer-dimer" in which the two oligonucleotides prime on each other. For this reason an improved forward primer, VH1FOR-2 was devised in which the two 3' nucleotides were removed from VH1FOR.

Thus, the preferred amplification conditions for mouse VH genes are as follows: the sample was made in a volume of 50-100 µl, 50-100 ng of DNA, VH1FOR-2 and VH1BACK primers (25 pmole of each), 250 µM of each deoxynucleotide triphosphate, 10 mM Tris.HCl, pH 8.8, 50 mM KCl, 1.5 mM MgCl₂, and 100 µg/ml gelatine. The sample was overlaid with paraffin oil, heated to 95 °C for 2 min, 65 °C for 2 min, and then to 72 °C: taq polymerase was added after the sample had reached the elongation temperature and the reaction continued for 2 min at 72 °C. The sample was subjected to a further 29 rounds of temperature cycling using the Techne PHC-1 programmable heating block.

The preferred amplification conditions for mouse V_k genes from genomic DNA are as follows: the sample treated as above except with V_x primers, for example VK3FOR and VK2BACK, and using a cycle of 94° C for one minute, 60° C for one minute and 72° C for one minute.

The conditions which were devised for genomic DNA are also suitable for amplification from the cDNA derived from mRNA from mouse spleen or mouse hybridoma.

Cloning and analysis of variable region genes

The reaction mixture was then extracted twice with 40 μ l of water-saturated diethyl ether. This was followed by a standard phenol extraction and ethanol precipitation as described in Example 1. The DNA pellet was then dissolved in 100 μ l 10 mM Tris.Cl, 0.1 mM EDTA.

Each reaction mixture containing a light chain variable domain encoding sequence was digested with SacI and Xhol (or with Pvull and BgIII) to enable it to be ligated into a suitable expression vector. Each reaction mixture containing a heavy chain variable domain encoding sequence was digested with PstI and BstEII for the same purpose.

The heavy chain variable genes isolated as above from a mouse hyperimmunised with lysozyme were cloned into M13VHPCR1 vector and sequenced. The complete sequences of 48 VH gene clones were determined (Figure 10). All but two of the mouse VH gene families were represented, with frequencies of: VA (1), IIIC (1), IIIB (8), IIIA (3), IIB (17), IIA (2), IB (12), IA (4). In 30 clones, the D segments could be assigned to families SP2 (14), FL16 (11) and Q52 (5), and in 38 clones the JH minigenes to families JH1 (3), JH2 (7), JH3 (14) and JH4 (14). The different sequences of CDR3 marked out each of the 48 clones as unique. Nine pseudogenes and 16 unproductive rearrangements were identified. Of the clones sequenced, 27 have open reading frames.

Thus the method is capable of generating a diverse repertoire of heavy chain variable genes from mouse spleen DNA.

Example 3

Cloning of rearranged variable genes from mRNA from human peripheral blood lymphocytes

Preparation of mRNA.

Human peripheral blood lymphocytes were purified and mRNA prepared directly (Method 1), or mRNA was prepared after addition of Epstein Barr virus (Method 2).

Method 1. 20 ml of heparinised human blood from a healthy volunteer was diluted with an equal volume of phosphate buffered saline (PBS) and distributed equally into 50 ml Falcon tubes. The blood was then underlayered with 15ml Ficoll Hypaque (Pharmacia 10-A-001-07). To separate the lymphocytes from the red blood cells, the tubes were spun for 10 minutes at 1800 rpm at room temperature in an IEC Centra 3E table centrifuge. The peripheral blood lymphocytes (PBL) were then collected from the interphase by aspiration with a Pasteur pipette. The cells were diluted with an equal volume of PBS and spun again at 1500 rpm for 15 minutes. The supernatant was aspirated, the cell pellet was resuspended in 1 ml PBS and the cells were distributed into two Eppendorf tubes.

Method 2. 40 ml human blood from a patient with HIV in the pre-AIDS condition was layered on Ficoll to separate the white cells (see Method 1 above). The white cells were then incubated in tissue culture medium for 4-5 days. On day 3, they were infected with Epstein Barr virus. The cells were pelleted (approx 2×10^7 cells) and washed in PBS.

The cells were pelleted again and lysed with 7 ml 5M guanidine isothiocyanate, 50 mM Tris, 10 mM EDTA, 0.1 mM dithiothreitol. The cells were vortexed vigorously and 7 volumes of 4M LiCl added. The mixture was incubated at 4° C for 15-20 hrs. The suspension was spun and the supernatant resuspended in 3M LiCl and centrifuged again. The pellet was dissolved in 2ml 0.1 % SDS, 10 mM Tris HCl and 1 mM EDTA. The suspension was frozen at -20° C, and thawed by vortexing for 20 s every 10 min for 45 min. A large white pellet was left behind and the clear supernatant was extracted with phenol chloroform, then with chloroform. The RNA was precipitated by adding 1/10 volume 3M sodium acetate and 2 vol ethanol and leaving overnight at -20° C. The pellet was suspended in 0.2 ml water and reprecipitated with ethanol. Aliquots for cDNA synthesis were taken from the ethanol precipitate which had been vortexed to create a fine suspension.

100 μ l of the suspension was precipitated and dissolved in 20 μ l water for cDNA synthesis [30] using 10 pmole of a HUFOR primer (see below) in final volume of 50 μ l. A sample of 5 μ l of the cDNA was

amplified as in Example 2 except using the primers for the human VH gene families (see below) using a cycle of 95 °C, 60 °C and 72 °C.

The back primers for the amplification of human DNA were designed to match the available human heavy and light chain sequences, in which the different families have slightly different nucleotide sequences at the 5' end. Thus for the human VH genes, the primers Hu2VHIBACK, HuVHIIBACK, Hu2VHIIIBACK and HuVH1VBACK were designed as back primers, and HUJH1FOR, HUJH2FOR and HUJH4FOR as forward primers based entirely in the variable gene. Another set of forward primers Hu1VHFOR, Hu2VHFOR, Hu3VHFOR, and Hu4VHFOR was also used, which were designed to match the human J-regions and the 5' end of the constant regions of different human isotopes.

Using sets of these primers it was possible to demonstrate a band of amplified ds cDNA by gel electrophoresis.

One such experiment was analysed in detail to establish whether there was a diverse repertoire in a patient with HIV infection. It is known that during the course of AIDS, that T-cells and also antibodies are greatly diminished in the blood. Presumably the repertoire of lymphocytes is also diminished. In this experiment, for the forward priming, an equimolar mixture of primers Hu1VHFOR, Hu2VHFOR, Hu3VHFOR, and Hu4VHFOR (in PCR 25 pmole of primer 5' ends) was used. For the back priming, the primers Hu2VHIBACK, HuVHIIBACK, Hu2VHIIIBACK and HuVH1VBACK were used separately in four separate primings. The amplified DNA from the separate primings was then pooled, digested with restriction enzymes PstI and BstEII as above, and then cloned into the vector M13VHPCR1 for sequencing. The sequences reveal a diverse repertoire (Fig. 11) at this stage of the disease.

For human V_x genes the primers HUJK1FOR, HUJK3FOR, HUJK4FOR and HUJK5FOR were used as forward primers and VK1BACK as back primer. Using these primers it was possible to see a band of amplified ds cDNA of the correct size by gel electrophoresis.

Example 4

Cloning of unrearranged variable gene genomic DNA from human peripheral blood lymphocytes

Human peripheral blood lymphocytes of a patient with non-Hodgkins lymphoma were prepared as in Example 3 (Method 1). The genomic DNA was prepared from the PBL using the technique described in Example 2 (Method 2). The VH region in the isolated genomic DNA was then amplified and cloned using the general protocol described in the first two paragraphs of the section headed "Amplification from RNA/DNA hybrid" in Example 1 above, except that during the annealing part of each cycle, the temperature was held at 55 °C and that 30 cycles were used. At the end of the 30 cycles, the reaction mixture was held at 60 °C for five minutes to ensure that complete elongation and renaturation of the amplified fragments had taken place.

The forward primer used was HuHep1FOR, which contains a SacI site. This primer is designed to anneal to the 3' end of the unrearranged human VH region gene, and in particular includes a sequence complementary to the last three codons in the VH region gene and nine nucleotides downstream of these three codons.

As the back primer, an equimolar mixture of HuOcta1BACK, HuOcta2BACK and HuOcta3BACK was used. These primers anneal to a sequence in the promoter region of the genomic DNA VH gene (see Figure 1). 5 μl of the amplified DNA was checked on 2% agarose gels in TBE buffer and stained with ethidium bromide. A double band was seen of about 620 nucleotides which corresponds to the size expected for the unrearranged VH gene. The ds cDNA was digested with SacI and cloned into an M13 vector for sequencing. Although there are some sequences which are identical, a range of different unrearranged human VH genes were identified (Figure 12).

Example 5

Cloning Variable Domains with Binding Activities from a Hybridoma

The heavy chain variable domain (VHLYS) of the D1.3 (anti-lysozyme) antibody was cloned into a vector similar to that described previously [42] but under the control of the lac z promoter, such that the VHLYS domain is attached to a pelB leader sequence for export into the periplasm. The vector was constructed by synthesis of the pelB leader sequence [43], using overlapping oligonucleotides, and cloning into a pUC 19 vector [35]. The VHLYS domain of the D1.3 antibody was derived from a cDNA clone [44] and the construct (pSW1) sequenced (Figure 13).

To express both heavy and light chain variable domains together, the light chain variable region (VKLYS) of the D1.3 antibody was introduced into the pSW1 vector, with a pelB signal sequence to give the construct pSW2 (Figure 14).

A strain of E. coli (BMH71-18) [45] was then transformed [46,47] with the plasmid pSW1 or pSW2, and 5 colonies resistant to ampicillin (100 µg/ml) were selected on a rich (2 x TY = per litre of water, 16g Bacto-tryptone, 10g yeast extract, 5g NaCl) plate which contained 1% glucose to repress the expression of variable domain(s) by catabolite repression.

The colonies were inoculated into 50 ml 2 x TY (with 1% glucose and 100 µg/ml ampicillin) and grown in flasks at 37 °C with shaking for 12-16 hr. The cells were centrifuged, the pellet washed twice with 50 mM 10 sodium chloride, resuspended in 2 x TY medium containing 100 µg/ml ampicillin and the inducer IPTG (1 mM) and grown for a further 30 hrs at 37 °C. The cells were centrifuged and the supernatant was passed through a Nalgene filter (0.45 µm) and then down a 1 - 5 ml lysozyme-Sepharose affinity column. (The column was derived by coupling lysozyme at 10 mg/ml to CNBr activated Sepharose.) The column was first washed with phosphate buffered saline (PBS), then with 50 mM diethylamine to elute the VHLYS domain 15 (from pSW1) or VHLYS in association with VKLYS (from pSW2).

The VHLYS and VKLYS domains were identified by SDS polyacrylamide electrophoresis as the correct size. In addition, N-terminal sequence determination of VHLYS and VKLYS isolated from a polyacrylamide gel showed that the signal peptide had been produced correctly. Thus both the Fv fragment and the VHLYS 20 domains are able to bind to the lysozyme affinity column, suggesting that both retain at least some of the affinity of the original antibody.

The size of the VHLYS domain was compared by FPLC with that of the Fv fragment on Superose 12. This indicates that the VHLYS domain is a monomer. The binding of the VHLYS and Fv fragment to lysozyme was checked by ELISA, and equilibrium and rapid reaction studies were carried out using fluorescence quench.

25 The ELISA for lysozyme binding was undertaken as follows:

(1) The plates (Dynatech Immulon) were coated with 200 µl per well of 300 µg/ml lysozyme in 50 mM NaHCO₃, pH 9.6 overnight at room temperature;

(2) The wells were rinsed with three washes of PBS, and blocked with 300 µl per well of 1% Sainsbury's instant dried skimmed milk powder in PBS for 2 hours at 37 °C;

30 (3) The wells were rinsed with three washes of PBS and 200 µl of VHLYS or Fv fragment (VHLYS associated with VKLYS) were added and incubated for 2 hours at room temperature;

(4) The wells were washed three times with 0.05% Tween 20 in PBS and then three times with PBS to remove detergent;

35 (5) 200 µl of a suitable dilution (1:1000) of rabbit polyclonal antisera raised against the Fv fragment in 2% skimmed milk powder in PBS was added to each well and incubated at room temperature for 2 hours;

(6) Washes were repeated as in (4);

(7) 200 µl of a suitable dilution (1:1000) of goat anti-rabbit antibody (ICN Immunochemicals) coupled to horse radish peroxidase, in 2% skimmed milk powder in PBS, was added to each well and incubated at 40 room temperature for 1 hour;

(8) Washes were repeated as in (4); and

(9) 200 µl 2,2'azino-bis(3-ethylbenzthiazolinesulphonic acid) [Sigma] (0.55 mg/ml, with 1 µl 20% hydrogen peroxide: water per 10 ml) was added to each well and the colour allowed to develop for up to 10 minutes at room temperature.

45 The reaction was stopped by adding 0.05% sodium azide in 50 mM citric acid pH 4.3. ELISA plates were read in a Titertek Multiscan plate reader. Supernatant from the induced bacterial cultures of both pSW1 (VHLYS domain) or pSW2 (Fv fragment) was found to bind to lysozyme in the ELISA.

The purified VHLYS and Fv fragments were titrated with lysozyme using fluorescence quench (Perkin Elmer LS5B Luminescence Spectrometer) to measure the stoichiometry of binding and the affinity constant 50 for lysozyme [48,49]. The titration of the Fv fragment at a concentration of 30 nM indicates a dissociation constant of 2.8 nM using a Scatchard analysis.

A similar analysis using fluorescence quench and a Scatchard plot was carried out for VHLYS, at a VHLYS concentration of 100 nM. The stoichiometry of antigen binding is about 1 mole of lysozyme per mole of VHLYS (calculated from plot). (The concentration of VH domains was calculated from optical 55 density at 280 nM using the typical extinction coefficient for complete immunoglobulins.) Due to possible errors in measuring low optical densities and the assumption about the extinction coefficient, the stoichiometry was also measured more carefully. VHLYS was titrated with lysozyme as above using fluorescence quench. To determine the concentration of VHLYS a sample of the stock solution was

removed, a known amount of norleucine added, and the sample subjected to quantitative amino acid analysis. This showed a stoichiometry of 1.2 mole of lysozyme per mole of VHLYS domain. The dissociation constant was calculated at about 12 nM.

The on-rates for VHLYS and Fv fragments with lysozyme were determined by stopped-flow analysis (HI Tech Stop Flow SHU machine) under pseudo-first order conditions with the fragment at a ten fold higher concentration than lysozyme [50]. The concentration of lysozyme binding sites was first measured by titration with lysozyme using fluorescence quench as above. The on rates were calculated per mole of binding site (rather than amount of VHLYS protein). The on-rate for the Fv fragment was found to be $2.2 \times 10^6 \text{ M}^{-1} \text{s}^{-1}$ at 25°C . The on-rate for the VHLYS fragment found to be $3.8 \times 10^6 \text{ M}^{-1} \text{s}^{-1}$ and the off-rate 0.075 s $^{-1}$ at 20°C . The calculated affinity constant is 19 nM. Thus the VHLYS binds to lysozyme with a dissociation constant of about 19 nM, compared with that of the Fv of 3 nM.

Example 6

15 Cloning complete variable domains with binding activities from mRNA or DNA of antibody-secreting cells

A mouse was immunised with hen egg white lysozyme (100 µg i.p. day 1 in complete Freunds adjuvant), after 14 days immunised i.p. again with 100 µg lysozyme with incomplete Freunds adjuvant, and on day 35 i.v. with 50 µg lysozyme in saline. On day 39, spleen was harvested. A second mouse was immunised with keyhole limpet haemocyanin (KLH) in a similar way. The DNA was prepared from the spleen according to Example 2 (Method 2). The VH genes were amplified according to the preferred method in Example 2.

Human peripheral blood lymphocytes from a patient infected with HIV were prepared as in Example 3 (Method 2) and mRNA prepared. The VH genes were amplified according to the method described in Example 3, using primers designed for human VH gene families.

After the PCR, the reaction mixture and oil were extracted twice with ether, once with phenol and once with phenol/CHCl₃. The double stranded DNA was then taken up in 50 µl of water and frozen. 5 µl was digested with PstI and BstEII (encoded within the amplification primers) and loaded on an agarose gel for electrophoresis. The band of amplified DNA at about 350 bp was extracted.

30 Expression of anti-lysozyme activities

The repertoire of amplified heavy chain variable domains (from mouse immunised with lysozyme and from human PBLs) was then cloned directly into the expression vector pSW1HPOLYMYC. This vector is derived from pSW1 except that the VHLYS gene has been removed and replaced by a polylinker restriction site. A sequence encoding a peptide tag was inserted (Figure 15). Colonies were toothpicked into 1 ml cultures. After induction (see Example 5 for details), 10 µl of the supernatant from fourteen 1 ml cultures was loaded on SDS-PAGE gels and the proteins transferred electrophoretically to nitrocellulose. The blot was probed with antibody 9E10 directed against the peptide tag.

40 The probing was undertaken as follows. The nitrocellulose filter was incubated in 3% bovine serum albumin (BSA)/TBS buffer for 20 min (10 x TBS buffer is 100 mM Tris.HCl, pH 7.4, 9% w/v NaCl). The filter was incubated in a suitable dilution of antibody 9E10 (about 1/500) in 3% BSA/TBS for 1 - 4 hrs. After three washes in TBS (100 ml per wash, each wash for 10 min), the filter was incubated with 1:500 dilution of anti-mouse antibody (peroxidase conjugated anti-mouse Ig (Dakopats)) in 3% BSA/TBS for 1 - 2 hrs. After three washes in TBS and 0.1% Triton X-100 (about 100 ml per wash, each wash for 10 min), a solution containing 10 ml chloronaphthol in methanol (3 mg/ml), 40 ml TBS and 50 µl hydrogen peroxide solution was added over the blot and allowed to react for up to 10 min. The substrate was washed out with excess water. The blot revealed bands similar in mobility to VHLYSMYC on the Western blot, showing that other VH domains could be expressed.

50 Colonies were then toothpicked individually into wells of an ELISA plate (200 µl) for growth and induction. They were assayed for lysozyme binding with the 9E10 antibody (as in Examples 5 and 7). Wells with lysozyme-binding activity were identified. Two positive wells (of 200) were identified from the amplified mouse spleen DNA and one well from the human cDNA. The heavy chain variable domains were purified on a column of lysozyme-Sepharose. The affinity for lysozyme of the clones was estimated by fluorescence quench titration as >50nM. The affinities of the two clones (VH3 and VH8) derived from the mouse genes were also estimated by stop flow analysis (ratio of k_{on}/k_{off}) as 12 nM and 27 nM respectively. Thus both these clones have a comparable affinity to the VHLYS domain. The encoded amino acid sequences of VH3 and VH8 are given in Figure 16, and that of the human variable domain in Figure 17.

A library of VH domains made from the mouse immunised with lysozyme was screened for both lysozyme and keyhole limpet haemocyanin (KLH) binding activities. Two thousand colonies were toothpicked in groups of five into wells of ELISA plates, and the supernatants tested for binding to lysozyme coated plates and separately to KLH coated plates. Twenty one supernatants were shown to have lysozyme binding activities and two to have KLH binding activities. A second expression library, prepared from a mouse immunised with KLH was screened as above. Fourteen supernatants had KLH binding activities and a single supernatant had lysozyme binding activity.

This shows that antigen binding activities can be prepared from single VH domains, and that immunisation facilitates the isolation of these domains.

10

Example 7

Cloning variable domains with binding activities by mutagenesis.

15 Taking a single rearranged VH gene, it may be possible to derive entirely new antigen binding activities by extensively mutating each of the CDRs. The mutagenesis might be entirely random, or be derived from pre-existing repertoires of CDRs. Thus a repertoire of CDR3s might be prepared as in the preceding examples by using "universal" primers based in the flanking sequences, and likewise repertoires of the other CDRs (singly or in combination). The CDR repertoires could be stitched into place in the flanking 20 framework regions by a variety of recombinant DNA techniques.

CDR3 appears to be the most promising region for mutagenesis as CDR3 is more variable in size and sequence than CDRs 1 and 2. This region would be expected to make a major contribution to antigen binding. The heavy chain variable region (VHLYS) of the anti-lysozyme antibody D1.3 is known to make several important contacts in the CDR3 region.

25 Multiple mutations were made in CDR3. The polymerase chain reaction (PCR) and a highly degenerate primer were used to make the mutations and by this means the original sequence of CDR3 was destroyed. (It would also have been possible to construct the mutations in CDR3 by cloning a mixed oligonucleotide duplex into restriction sites flanking the CDR or by other methods of site-directed mutagenesis). Mutants expressing heavy chain variable domains with affinities for lysozyme were screened and those with 30 improved affinities or new specificities were identified.

The source of the heavy chain variable domain was an M13 vector containing the VHLYS gene. The body of the sequence encoding the variable region was amplified using the polymerase chain reaction (PCR) with the mutagenic primer VHMUT1 based in CDR3 and the M13 primer which is based in the M13 vector backbone. The mutagenic primer hypermutates the central four residues of CDR3 (Arg-Asp-Tyr-Arg).

35 The PCR was carried out for 25 cycles on a Techne PHC-1 programmable heat block using 100 ng single stranded M13mp19SW0 template, with 25 pmol of VHMUT1 and the M13 primer, 0.5 mM each dNTP, 67mM Tris.HCl, pH 8.8, 10 mM MgCl₂, 17 mM (NH₄)₂SO₄, 200 µg/ml gelatine and 2.5 units Taq polymerase in a final volume of 50 µl. The temperature regime was 95 °C for 1.5 min, 25 °C for 1.5 min and 72 °C for 3 min (However a range of PCR conditions could be used). The reaction products were extracted 40 with phenol/chloroform, precipitated with ethanol and resuspended in 10 mM Tris. HCl and 0.1 mM EDTA, pH 8.0.

The products from the PCR were digested with PstI and BstEII and purified on a 1.5% LGT agarose gel in Tris acetate buffer using Geneclean (Bio 101, LaJolla). The gel purified band was ligated into pSW2HPOLY (Figure 19). (This vector is related to pSW2 except that the body of the VHLYS gene has 45 been replaced by a polylinker.) The vector was first digested with BstEII and PstI and treated with calf-intestinal phosphatase. Aliquots of the reaction mix were used to transform E. coli BMH 71-18 to ampicillin resistance. Colonies were selected on ampicillin (100 µg/ml) rich plates containing glucose at 0.8% w/v.

Colonies resulting from transfection were picked in pools of five into two 96 well Corning microtitre plates, containing 200 µl 2 x TY medium and 100 µl TY medium, 100 µg/ml ampicillin and 1% glucose. 50 The colonies were grown for 24 hours at 37 °C and then cells were washed twice in 200 µl 50 mM NaCl, pelleting the cells in an IEC Centra-3 bench top centrifuge with microtitre plate head fitting. Plates were spun at 2,500 rpm for 10 min at room temperature. Cells were resuspended in 200 µl 2 x TY, 100 µg/ml ampicillin and 1 mM IPTG (Sigma) to induce expression, and grown for a further 24 hr.

Cells were spun down and the supernatants used in ELISA with lysozyme coated plates and anti-idiotypic sera (raised in rabbits against the Fv fragment of the D1.3 antibody). Bound anti-idiotypic serum was detected using horse radish peroxidase conjugated to anti-rabbit sera (ICN Immunochemicals). Seven of the wells gave a positive result in the ELISA. These pools were restreaked for single colonies which were 55 picked, grown up, induced in microtitre plates and rescreened in the ELISA as above. Positive clones were

grown up at the 50 ml scale and expression was induced. Culture supernatants were purified as in Example 5 on columns of lysozyme-Sepharose and eluates analysed on SDS-PAGE and staining with Page Blue 90 (BDH). On elution of the column with diethylamine, bands corresponding to the VHLYS mutant domains were identified, but none to the VKLYS domains. This suggested that although the mutant domains could bind to lysozyme, they could no longer associate with the VKLYS domains.

For seven clones giving a positive reaction in ELISA, plasmids were prepared and the VKLYS gene excised by cutting with EcoRI and religating. Thus the plasmids should only direct the expression of the VHLYS mutants. 1.5 ml cultures were grown and induced for expression as above. The cells were spun down and supernatant shown to bind lysozyme as above. (Alternatively the amplified mutant VKLYS genes could have been cloned directly into the pSW1HPOLY vector for expression of the mutant activities in the absence of VKLYS.)

An ELISA method was devised in which the activities of bacterial supernatants for binding of lysozyme (or KLH) were compared. Firstly a vector was devised for tagging of the VH domains at its C-terminal region with a peptide from the c-myc protein which is recognised by a monoclonal antibody 9E10. The vector was derived from pSW1 by a BstEII and SmaI double digest, and ligation of an oligonucleotide duplex made from

5' GTC ACC GTC TCC TCA GAA CAA AAA CTC ATC TCA GAA GAG GAT
CTG AAT TAA TAA 3' and

5' TTA TTA ATT CAG ATC CTC TTC TGA GAT GAG TTT TTG TTC TGA
GGA GAC G 3'.

The VHLYSMYC protein domain expressed after induction was shown to bind to lysozyme and to the 9E10 antibody by ELISA as follows:

- (1) Falcon (3912) flat bottomed wells were coated with 180 µl lysozyme (3 mg/ml) or KLH (50 µg/ml) per well in 50 mM NaHCO₃, pH 9.6, and left to stand at room temperature overnight;
- (2) The wells were washed with PBS and blocked for 2 hrs at 37 °C with 200 µl 2% Sainsbury's instant dried skimmed milk powder in PBS per well;
- (3) The Blocking solution was discarded, and the walls washed out with PBS (3 washes) and 150 µl test solution (supernatant or purified tagged domain) pipetted into each well. The sample was incubated at 37 °C for 2 hrs;
- (4) The test solution was discarded, and the wells washed out with PBS (3 washes). 100 µl of 4 µg/ml purified 9E10 antibody in 2% Sainsbury's instant dried skimmed milk powder in PBS was added, and incubated at 37 °C for 2 hrs;
- (5) The 9E10 antibody was discarded, the wells washed with PBS (3 washes). 100 µl of 1/500 dilution of anti-mouse antibody (peroxidase conjugated anti-mouse Ig (Dakopats)) was added and incubated at 37 °C for 2 hrs;
- (6) The second antibody was discarded and wells washed three times with PBS; and
- (7) 100 µl 2,2'-azino-bis(3-ethylbenzthiazolinesulphonic acid) [Sigma] (0.55 mg/ml, with 1 µl 20% hydrogen peroxide: water per 10 ml) was added to each well and the colour allowed to develop for up to 10 minutes at room temperature.

The reaction was stopped by adding 0.05% sodium azide in 50 mM citric acid, pH 4.3. ELISA plates were read in an Titertek Multiscan plate reader.

The activities of the mutant supernatants were compared with VHLYS supernatant by competition with the VHLYSMYC domain for binding to lysozyme. The results show that supernatant from clone VHLYS-MUT59 is more effective than wild type VHLYS supernatant in competing for VHLYSMYC. Furthermore, Western blots of SDS-PAGE aliquots of supernatant from the VHLYS and VHLYSMUT59 domain (using anti-Fv antisera) indicated comparable amounts of the two samples. Thus assuming identical amounts of VHLYS and VHLYSMUT59, the affinity of the mutant appears to be greater than that of the VHLYS domain.

To check the affinity of the VHLYSMUT59 domain directly, the clone was grown at the 1l scale and 200-300 µg purified on lysozyme-Sepharose as in Example 5. By fluorescence quench titration of samples of VHLYS and VHLYSMUT59, the number of binding sites for lysozyme were determined. The samples of VHLYS and VHLYSMUT59 were then compared in the competition ELISA with VHLYSMYC over two orders of magnitude. In the competition assay each microtitre well contained a constant amount of VHLYSMYC (approximately 0.6 µg VHLYSMYC). Varying amounts of VHLYS or VHLYSMUT59 (3.8 µM in lysozyme binding sites) were added (0.166 - 25 µl). The final volume and buffer concentration in all wells was

constant. 9E10 (anti-myc) antibody was used to quantitate bound VHLYSMYC in each assay well. The % inhibition of VHLYSMYC binding was calculated for each addition of VHLYS or VHLYSMUT59, after subtraction of background binding. Assays were carried out in duplicate. The results indicate that VHLYS-MUT59 has a higher affinity for lysozyme than VHLYS.

5 The VHLYSMUT59 gene was sequenced (after recloning into M13) and shown to be identical to the VHLYS gene except for the central residues of CDR3 (Arg-Asp-Tyr-Arg). These were replaced by Thr-Gln-Arg-Pro: (encoded by ACACAAAGGCCA).

10 A library of 2000 mutant VH clones was screened for lysozyme and also for KLH binding (toothpicking 5 colonies per well as described in Example 6). Nineteen supernatants were identified with lysozyme binding activities and four with KLH binding activities. This indicates that new specificities and improved affinities can be derived by making a random repertoire of CDR3.

Example 8

15 Construction and expression of double domain for lysozyme binding.

The finding that single domains have excellent binding activities should allow the construction of strings of domains (concatamers). Thus, multiple specificities could be built into the same molecule, allowing binding to different epitopes spaced apart by the distance between domain heads. Flexible linker regions 20 could be built to space out the domains. In principle such molecules could be devised to have exceptional specificity and affinity.

Two copies of the cloned heavy chain variable gene of the D1.3 antibody were linked by a nucleotide sequence encoding a flexible linker
 Gly-Gly-Gly-Ala-Pro-Ala-Ala-Ala-Pro-Ala-Gly-Gly-Gly-
 25 (by several steps of cutting, pasting and site directed mutagenesis) to yield the plasmid pSW3 (Figure 20). The expression was driven by a lacZ promoter and the protein was secreted into the periplasm via a *peB* leader sequence (as described in Example 5 for expression of pSW1 and PSW2). The protein could be purified to homogeneity on a lysozyme affinity column. On SDS polyacrylamide gels, it gave a band of the right size (molecular weight about 26,000). The protein also bound strongly to lysozyme as detected by
 30 ELISA (see Example 5) using anti-idiotypic antiserum directed against the Fv fragment of the D1.3 antibody to detect the protein. Thus, such constructs are readily made and secreted and at least one of the domains binds to lysozyme.

Example 9

35 Introduction of cysteine residue at C-terminal end of VHLYS

A cysteine residue was introduced at the C-terminus of the VHLYS domain in the vector pSW2. The cysteine was introduced by cleavage of the vector with the restriction enzymes *Bst*I and *Sma*I (which 40 excises the C-terminal portion of the J segment) and ligation of a short oligonucleotide duplex
 5' GTC ACC GTC TCC TCA TGT TAA TAA 3' and
 5' TTA TTA ACA TGA GGA GAC G 3'.

By purification on an affinity column of lysozyme Sepharose it was shown that the VHLYS-Cys domain was expressed in association with the VKLYS variable domain, but the overall yields were much lower than the 45 wild type Fv fragment. Comparison of non-reducing and reducing SDS polyacrylamide gels of the purified Fv-Cys protein indicated that the two VH-Cys domains had become linked through the introduced cysteine residue.

Example 10

50 Linking of VH domain with enzyme

Linking of enzyme activities to VH domains should be possible by either cloning the enzyme on either the N-terminal or the C-terminal side of the VH domain. Since both partners must be active, it may be 55 necessary to design a suitable linker (see Example 8) between the two domains. For secretion of the VH-enzyme fusion, it would be preferable to utilise an enzyme which is usually secreted. In Figure 21, there is shown the sequence of a fusion of a VH domain with alkaline phosphatase. The alkaline phosphatase gene was cloned from a plasmid carrying the *E. coli* alkaline phosphatase gene in a plasmid pEK48 [51] using

the polymerase chain reaction. The gene was amplified with the primers

5' CAC CAC GGT CAC CGT CTC CTC ACG GAC ACC AGA AAT GCC TGT
 5 TCT G 3' and
 5' GCG AAA ATT CAC TCC CGG GCG CGG TTT TAT TTC 3'.

The gene was introduced into the vector pSW1 by cutting at BstEII and SmaI. The construction (Figure 21)
 10 was expressed in *E. coli* strain BMH71-18 as in Example 5 and screened for phosphatase activity using 1 mg/ml p-nitrophenylphosphate as substrate in 10mM diethanolamine and 0.5 mM MgCl², pH 9.5) and also on SDS polyacrylamide gels which had been Western blotted (detecting with anti-idiotypic antiserum). No evidence was found for the secretion of the linked VHLYS-alkaline phosphatase as detected by Western blots (see Example 5), or for secretion of phosphatase activity.

15 However when the construct was transfected into a bacterial strain BL21DE3 [52] which is deficient in proteases, a band of the correct size (as well as degraded products) was detected on the Western blots. Furthermore phosphatase activity could now be detected in the bacterial supernatant. Such activity is not present in supernatant from the strain which had not been transfected with the construct.

20 A variety of linker sequences could then be introduced at the BstEII site to improve the spacing between the two domains.

Example 11

Coexpression of VH domains with Vk repertoire

25 A repertoire of Vx genes was derived by PCR using primers as described in Example 2 from DNA prepared from mouse spleen and also from mouse spleen mRNA using the primers VK3FOR and VK2BACK and a cycle of 94°C for 1 min, 60°C for 1 min, 72°C for 2 min. The PCR amplified DNA was fractionated on the agarose gel, the band excised and cloned into a vector which carries the VHLYS domain
 30 (from the D1.3 antibody), and a cloning site (Sacl and Xhol) for cloning of the light chain variable domains with a myc tail (pSW1VHLYS-VKPOLYMYC, Figure 22).

Clones were screened for lysozyme binding activities as described in Examples 5 and 7 via the myc tag on the light chain variable domain, as this should permit the following kinds of Vx domains to be identified:

- 35 (1) those which bind to lysozyme in the absence of the VHLYS domain;
 (2) those which associate with the heavy chain and make no contribution to binding of lysozyme; and
 (3) those which associate with the heavy chain and also contribute to binding of lysozyme (either helping or hindering).

40 This would not identify those Vx domains which associated with the VHLYS domain and completely abolished its binding to lysozyme.

In a further experiment, the VHLYS domain was replaced by the heavy chain variable domain VH3 which had been isolated from the repertoire (see Example 6), and then the Vx domains cloned into the vector. (Note that the VH3 domain has an internal Sacl site and this was first removed to allow the cloning of the Vx repertoire as Sacl-Xhol fragments.)

45 By screening the supernatant using the ELISA described in Example 6, bacterial supernatants will be identified which bind lysozyme.

Example 12

High expression of VH domains.

By screening several clones from a VH library derived from a mouse immunised with lysozyme via a Western blot, using the 9E10 antibody directed against the peptide tag, one clone was noted with very high levels of expression of the domain (estimated as 25 - 50 mg/l). The clone was sequenced to determine the nature of the sequence. The sequence proved to be closely related to that of the VHLYS domain, except with a few amino acid changes (Figure 23). The result was unexpected, and shows that a limited number of amino acid changes, perhaps even a single amino acid substitution, can cause greatly elevated levels of expression.

By making mutations of the high expressing domain at these residues, it was found that a single amino acid change in the VHLYS domain(Asn 35 to His) is sufficient to cause the domain to be expressed at high levels.

5 CONCLUSION

It can thus be seen that the present invention enables the cloning, amplification and expression of heavy and light chain variable domain encoding sequences in a much more simple manner than was previously possible. It also shows that isolated variable domains or such domains linked to effector molecules are unexpectedly useful.

10 It will be appreciated that the present invention has been described above by way of example only and that variations and modifications may be made by the skilled person without departing from the scope of the invention.

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Claims

1. A method of cloning sequences (target sequences) each containing a sequence encoding at least part of an immunoglobulin variable domain, which method comprises providing a sample repertoire of nucleic acid containing target sequences, and using forward and back primers in the process of copying and cloning of the target sequences for expression of a repertoire of proteins each comprising at least part of an immunoglobulin variable domain, the forward primer being specific for a sequence at or adjacent the 3' end of the sense strand of each of the target sequences, the back primer being specific for a sequence at or adjacent the 3' end of the antisense strand of each of the target sequences.
 15
2. A method according to claim 1 which method comprises:
 - (a) providing a sample repertoire of double-stranded nucleic acid containing target sequences;
 - (b) causing the two strands of the doubled-stranded nucleic acid to be separated;
 - (c) annealing to the sample a forward and a back oligonucleotide primer, the forward primer being specific for a sequence at or adjacent the 3' end of the sense strand of each of the target sequences, the back primer being specific for a sequence at or adjacent the 3' end of the antisense strand of each of the target sequences, under conditions which allow the primers to hybridize specifically to the nucleic acid;
 - (d) treating the annealed sample with a DNA polymerase enzyme in the presence of deoxyribonucleoside triphosphates under conditions which cause primer extension to take place, thereby producing double-stranded nucleic acid;
 - (e) repeating steps (b) to (d), thereby producing some double-stranded DNA (product DNA) containing only the target sequences;
 - (f) cloning product DNA into expression vectors for expression of a repertoire of proteins each comprising at least part of an immunoglobulin variable domain.
 25
3. A method according to claim 2 wherein steps (b) to (d) are repeated a plurality of times before step (f).
 40
4. A method according to claim 1, which comprises:
 - (a) providing a repertoire of mRNA;
 - (b) annealing to the mRNA an oligonucleotide primer specific for a sequence at or adjacent the 3' end of each of the target sequences on the sense strands, under conditions which allow the primer to hybridize specifically to the nucleic acid;
 - (c) treating the primer-annealed mRNA with a polymerase enzyme in the presence of deoxyribonucleoside triphosphates under conditions which cause primer extension to take place, thereby producing antisense cDNA;
 - (d) annealing to the cDNA an oligonucleotide primer specific for a sequence at or adjacent the 3' end of each of the target sequences on the antisense strands, under conditions which allow the primer to hybridize specifically to the nucleic acid;
 - (e) treating the primer-annealed cDNA with a polymerase enzyme in the presence of deoxyribonucleoside triphosphates under conditions which cause primer extension to take place, thereby producing double-stranded DNA (product DNA);
 - (f) cloning product DNA into expression vectors for expression of a repertoire of proteins each comprising at least part of an immunoglobulin variable domain.
 45
5. A method according to claim 4 wherein, after step (e) the following steps are performed before step (f):
 - (a)
 - (b)
 - (c)
 - (d)
 - (e)
 - (f)
 50

(i) causing the two strands of the product DNA to be separated;
5 (ii) annealing to the separated strands a forward and a back oligonucleotide primer, the forward primer being specific for a sequence at or adjacent the 3' end of the sense strand of each of the target sequences, the back primer being specific for a sequence at or adjacent the 3' end of the antisense strand of each of the target sequences, under conditions which allow the primers to hybridize specifically to the nucleic acid;
10 (iii) treating the annealed sample with a DNA polymerase enzyme in the presence of deoxyribonucleoside triphosphates under conditions which cause primer extension to take place, thereby producing double-stranded nucleic acid.

- 15 6. A method according to any one of claims 1 to 5 wherein the back primer is specific for a sequence at or adjacent the 3' end of the antisense strand of the sequences which are contained in the target sequences and which each encode at least part of an immunoglobulin variable domain.
- 20 7. A method according to any one of claims 1 to 6 wherein the sample repertoire of double-stranded nucleic acid is derived from lymphocytes.
8. A method according to claim 7 wherein the lymphocytes are derived from an animal or human mounting an immune response to an antigen.
- 25 9. A method according to claim 7 wherein the lymphocytes are derived from a patient with an autoimmune disease.
10. A method according to claim 1 wherein the sample repertoire of nucleic acid is derived from rearranged immunoglobulin variable region genes.
- 25 11. A method according to claim 1 wherein the sample repertoire of nucleic acid is genomic DNA.
- 30 12. A method according to claim 1 wherein the sample repertoire of nucleic acid is derived from unrearranged immunoglobulin variable region genes.
13. A method according to any one of claims 1 to 12 wherein the target sequence contains a sequence encoding a variable domain from an immunoglobulin heavy chain.
- 35 14. A method according to claim 13 wherein the product DNA is inserted into an expression vector for expression of single domain ligands selectable by their binding affinity for antigen.
15. A method according to any one of claims 1 to 13 wherein product DNA is inserted into an expression vector for expression of antibodies or antibody fragments selectable by their binding affinity for antigen.
- 40 16. A method according to any one of claims 1 to 13 wherein the product DNA is inserted into an expression vector for expression alone.
17. The method of any one of claims 1 to 13 wherein the product DNA is inserted into an expression vector for expression in combination with a complementary variable domain.
- 45 18. A method according to any one of claims 1 to 13 wherein the product DNA is inserted into an expression vector already containing sequences encoding one or more constant domains for expression.
- 50 19. A method according to any one of claims 1 to 13 wherein the product DNA is inserted into an expression vector for expression as fusion proteins.
20. A method according to any one of claims 1 to 13 wherein the product DNA is inserted into an expression vector for expression with peptide tags.
- 55 21. A method according to any one of claims 1 to 13 wherein product DNA containing sequences encoding at least immunoglobulin heavy chain variable domains and product DNA containing sequences

encoding at least immunoglobulin light chain variable domains are inserted into expression vectors for expression of a combinatorial repertoire of complementary variable domains.

22. A method according to claim 21 wherein the product DNA is inserted into an expression vector already
5 containing sequences encoding one or more constant domains for expression.
23. A method according to claim 21 wherein product DNA is inserted into expression vectors for expression
as fusion proteins.
- 10 24. A method according to claim 21 wherein the product DNA is inserted into an expression vector for
expression with peptide tags.
25. A method according to any one of claims 1 to 24 wherein the forward and back primers are provided as
single oligonucleotides.
15
26. A method according to any one of claims 1 to 24 wherein the forward primers are supplied as a mixture
of oligonucleotides.
27. A method according to any one of claims 1 to 24 wherein the back primers are supplied as a mixture of
20 oligonucleotides.
28. A method according to any one of claims 1 to 27 wherein each primer includes a sequence encoding a
restriction enzyme recognition site.
- 25 29. A method according to claim 28 wherein the restriction enzyme recognition site is located in the
sequence which is annealed to the nucleic acid.
30. A method according to claim 1 wherein the back primer is a general primer useful for cloning a desired
antibody specificity from a specific species.
30
31. A method according to claim 1 wherein the back primer is a mixture of primers having a variety of
sequences designed to be complementary to the various families of VH, Vk or V sequences.
32. An expression library comprising a repertoire of nucleic acid sequences each encoding at least part of
35 an immunoglobulin variable domain.

Patentansprüche

1. Verfahren zum Klonieren von Sequenzen (Zielsequenzen), die jeweils eine Sequenz enthalten, die für
40 zumindest einen Teil einer variablen Immunoglobulindomäne kodieren, welches Verfahren die Schaf-
fung einer Probensammlung von Zielsequenzen enthaltenden Nukleinsäuren und die Verwendung von
Vorwärts- und Rückwärts-Primern beim Verfahren zum Kopieren und Klonieren der Zielsequenzen zur
Expression einer Sammlung von Proteinen umfaßt, von denen jedes zumindest einen Teil einer variablen
45 Immunoglobulindomäne aufweist, wobei der Vorwärtsprimer für eine Sequenz am oder im Bereich des 3'-Endes des "sense"-Strangs einer jeden der Zielsequenzen spezifisch ist und der Rückwärtsprimer für eine Sequenz am oder im Bereich des 3'-Endes des "antisense"-Strangs einer jeden der Zielsequenzen spezifisch ist.
2. Verfahren nach Anspruch 1, welches Verfahren umfaßt:
50 (a) das Schaffen einer Probensammlung von Zielsequenzen enthaltenden doppelstrangigen Nuklein-
säuren;
(b) das Bewirken der Trennung der beiden Stränge der doppelstrangigen Nukleinsäure;
(c) das Anlagern eines Vorwärts- und eines Rückwärtsoligonukleotidprimers an die Probe, wobei der Vorwärtsprimer für eine Sequenz am oder im Bereich des 3'-Endes des "sense"-Strangs einer jeden der Zielsequenzen spezifisch ist und der Rückwärtsprimer für eine Sequenz am oder im Bereich des 3'-Endes des "antisense"-Strangs einer jeden der Zielsequenzen spezifisch ist, unter Bedingungen, die das spezifische Hybridisieren der Primer an die Nukleinsäure ermöglichen;

- (d) das Behandeln der angelagerten Probe mit einem DNA-Polymeraseenzym in Gegenwart eines Desoxynukleosidtriphosphats unter Bedingungen, die bewirken, daß Primerextension stattfindet, wodurch doppelstrangige Nukleinsäure erzeugt wird;
- 5 (e) das Wiederholen der Schritte (b) bis (d), wodurch etwas doppelstrangige DNA (Produkt-DNA) erzeugt wird, die nur die Zielsequenzen enthält;
- (f) das Klonieren von Produkt-DNA in Expressionsvektoren zur Expression einer Sammlung von Proteinen, die jeweils zumindest einen Teil einer variablen Immunoglobulindomäne umfassen.
- 10 3. Verfahren nach Anspruch 2, worin die Schritte (b) bis (d) vor Schritt (f) mehrere Male wiederholt werden.
- 15 4. Verfahren nach Anspruch 1, welches umfaßt:
- (a) das Schaffen einer mRNA-Sammlung;
- (b) das Anlagern eines Oligonukleotidprimers an die mRNA, der für eine Sequenz am oder im Bereich des 3'-Endes einer jeden der Zielsequenzen an den "sense"-Strängen spezifisch ist, unter Bedingungen, die die spezifische Hybridisierung des Primers an die Nukleinsäure ermöglichen;
- 20 (c) das Behandeln der primerangelagerten mRNA mit einem Polymeraseenzym in Gegenwart von Desoxynukleosidtriphosphaten unter Bedingungen, die bewirken, daß Primerextension stattfindet, wodurch "antisense"-cDNA erzeugt wird;
- (d) das Anlagern eines Oligonukleotidprimers an die cDNA, der für eine Sequenz am oder angrenzend am 3'-Ende einer jeden der Zielsequenzen an den "antisense"-Strängen spezifisch ist, unter Bedingungen, die die spezifische Hybridisierung des Primers an die Nukleinsäure ermöglichen;
- 25 (e) das Behandeln der primerangelagerten cDNA mit einem Polymeraseenzym in Gegenwart von Desoxynukleosidtriphosphaten unter Bedingungen, die bewirken, daß Primerextension stattfindet, wodurch doppelstrangige DNA (Produkt-DNA) erzeugt wird;
- (f) das Klonieren von Produkt-DNA in Expressionsvektoren zur Expression einer Sammlungen von Proteinen, die jeweils zumindest einen Teil einer variablen Immunoglobulindomäne umfassen.
- 30 5. Verfahren nach Anspruch 4, worin nach Schritt (e) die folgenden Schritte vor Schritt (f) durchgeführt werden:
- (i) das Bewirken der Trennung der beiden Stränge der Produkt-DNA;
- (ii) das Anlagern eines Vorwärts- und eines Rückwärtsoligonukleotidprimers an die getrennten Stränge, wobei der Vorwärtsprimer für eine Sequenz am oder im Bereich des 3'-Endes des "sense"-Stranges einer jeden der Zielsequenzen spezifisch ist und der Rückwärtsprimer für eine Sequenz am oder im Bereich des 3'-Endes des "antisense"-Stranges einer jeden der Zielsequenzen spezifisch ist, unter Bedingungen, die das spezifische Hybridisieren der Primer an die Nukleinsäure ermöglichen;
- 35 (iii) das Behandeln der angelagerten Probe mit einem DNA-Polymeraseenzym in Gegenwart von Desoxynukleosidtriphosphaten unter Bedingungen, die bewirken, daß Primerextension stattfindet, wodurch doppelstrangige Nukleinsäure erzeugt wird.
- 40 6. Verfahren nach einem der Ansprüche 1 bis 5, worin der Rückwärtsprimer für eine Sequenz am oder im Bereich des 3'-Endes des "antisense"-Stranges der Sequenzen spezifisch ist, die in den Zielsequenzen enthalten sind und von denen jede für zumindest einen Teil einer variablen Immunoglobulindomäne kodiert.
7. Verfahren nach einem der Ansprüche 1 bis 6, worin die Probensammlung von doppelstrangigen Nukleinsäuren von Lymphozyten abgeleitet ist.
- 50 8. Verfahren nach Anspruch 7, worin die Lymphozyten von einem Tier oder Menschen stammen, der eine Immunreaktion auf ein Antigen zeigt.
9. Verfahren nach Anspruch 7, worin die Lymphozyten von einem Patienten mit einer Autoimmunerkrankung stammen.
- 55 10. Verfahren nach Anspruch 1, worin die Nukleinsäurenprobensammlung von umorientierten variablen Immunoglobulindomänenengenen abgeleitet ist.

11. Verfahren nach Anspruch 1, worin die Nukleinsäureprobensammlung genomische DNA ist.
12. Verfahren nach Anspruch 1, worin die Nukleinsäureprobensammlung von nicht umorientierten variablen Immunoglobulindomänenengenen abgeleitet ist.
5
13. Verfahren nach einem der Ansprüche 1 bis 12, worin die Zielsequenz eine Sequenz enthält, die für eine variable Domäne der schweren Kette eines Immunoglobulins kodiert.
14. Verfahren nach Anspruch 13, worin die Produkt-DNA in einen Expressionsvektor zur Expression von Einzeldomänenliganden eingesetzt wird, die nach ihrer Bindungsaffinität für Antigen auswählbar sind.
10
15. Verfahren nach einem der Ansprüche 1 bis 13, worin Produkt-DNA in einen Expressionsvektor zur Expression von Antikörpern oder Antikörperfragmenten eingesetzt wird, die nach ihrer Bindungsaffinität für Antigen auswählbar sind.
15
16. Verfahren nach einem der Ansprüche 1 bis 13, worin die Produkt-DNA in einen Expressionvektor nur zur Expression eingesetzt wird.
17. Verfahren nach einem der Ansprüche 1 bis 13, worin die Produkt-DNA in einen Expressionvektor zur Expression in Kombination mit einer komplementären variablen Domäne eingesetzt wird.
20
18. Verfahren nach einem der Ansprüche 1 bis 13, worin die Produkt-DNA in einen Expressionvektor eingesetzt wird, der bereits Sequenzen enthält, die für eine oder mehrere konstante Domänen zur Expression kodieren.
25
19. Verfahren nach einem der Ansprüche 1 bis 13, worin die Produkt-DNA in einen Expressionvektor zur Expression als Fusionsproteine eingesetzt wird.
20. Verfahren nach einem der Ansprüche 1 bis 13, worin die Produkt-DNA in einen Expressionsvektor zur Expression mit Peptidanhangseln eingesetzt wird.
30
21. Verfahren nach einem der Ansprüche 1 bis 13, worin Produkt-DNA, die Sequenzen enthält, die zumindest für variable Domänen der schweren Kette von Immunoglobulinen kodieren, und Produkt-DNA, die Sequenzen enthält, die zumindest für variable Domänen der leichten Kette von Immunoglobulinen kodieren, zur Expression einer Kombinationssammlung von komplementären variablen Domänen in Expressionvektoren eingesetzt wird.
35
22. Verfahren nach Anspruch 21, worin die Produkt-DNA zur Expression in einen Expressionvektor eingesetzt wird, der bereits Sequenzen enthält, die für eine oder mehrere konstante Domänen kodieren.
40
23. Verfahren nach Anspruch 21, worin Produkt-DNA in Expressionsvektoren zur Expression als Fusionsproteine eingesetzt wird.
24. Verfahren nach Anspruch 21, worin Produkt-DNA in einen Expressionsvektor zur Expression mit Peptidanhangseln eingesetzt wird.
45
25. Verfahren nach einem der Ansprüche 1 bis 24, worin die Vorwärts- und Rückwärtsprimer als einzelne Oligonukleotide vorhanden sind.
26. Verfahren nach einem der Ansprüche 1 bis 24, worin die Vorwärtsprimer als eine Mischung aus Oligonukleotiden zugeführt werden.
50
27. Verfahren nach einem der Ansprüche 1 bis 24, worin die Rückwärtsprimer als eine Mischung aus Oligonukleotiden zugeführt werden.
28. Verfahren nach einem der Ansprüche 1 bis 27, worin jeder Primer eine Sequenz umfaßt, die für eine Restriktionsenzymmerkennungsstelle kodiert.
55

29. Verfahren nach Anspruch 28, worin die Restriktionsenzymerkennungsstelle sich in der Sequenz befindet, die an die Nukleinsäure angelagert ist.
30. Verfahren nach Anspruch 1, worin der Rückwärtsprimer ein allgemeiner Primer ist, der zum Klonieren einer gewünschten Antikörperspezifität von einer spezifischen Spezies nützlich ist.
5
31. Verfahren nach Anspruch 1, worin der Rückwärtsprimer eine Mischung aus Primern mit einer Vielzahl von Sequenzen ist, die so konstruiert sind, daß sie komplementär zu den verschiedenen Familien von VH-, Vk- oder V-Sequenzen sind.
10
32. Expressionskollektion, die eine Sammlung von Nukleinsäuresequenzen umfaßt, von denen jede für zumindest einen Teil einer variablen Immunoglobulindomäne kodiert.

Revendications

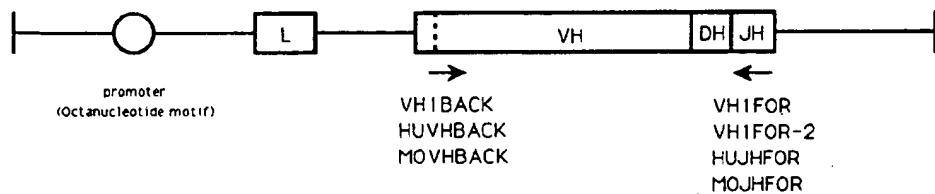
1. Méthode de clonage de séquences (séquences cibles), chacune contenant une séquence codant au moins une partie d'un domaine variable d'immunoglobuline , laquelle méthode consiste à produire un répertoire d'échantillons de séquences cibles contenant de l'acide nucléique et à utiliser des amorces vers l'avant et vers l'arrière dans le processus de copiage et de clonage des séquences cibles pour l'expression d'un répertoire des protéines, chacune comprenant au moins une partie d'un domaine variable d'immunoglobuline , l'amorce vers l'avant étant spécifique d'une séquence à ou près de l'extrémité 3' du brin de sens de chacune des séquences cibles, l'amorce vers l'arrière étant spécifique d'une séquence à ou adjacente à l'extrémité 3' du brin anti-sens de chacune des séquences cibles.
15
2. Méthode selon la revendication 1, laquelle consiste à :
 - (a) prévoir un répertoire d'échantillons de séquences cibles contenant de l'acide nucléique à deux brins ;
 - (b) forcer les deux brins de l'acide nucléique à deux brins à se séparer ;
 - (c) recuire, sur l'échantillon ,une amorce d'oligonucléotides vers l'avant et vers l'arrière, l'amorce vers l'avant étant spécifique d'une séquence à ou à proximité de l'extrémité 3' du brin de sens de chacune des séquences cibles, l'amorce vers l'arrière étant spécifique d'une séquence à ou adjacente à l'extrémité 3' du brin de l'anti-sens de chacune des séquences cibles, dans des conditions qui permettent aux amorces de s'hybrider spécifiquement à l'acide nucléique ;
20
 - (d) traiter l'échantillon recuit avec une enzyme d'ADN polymérase en présence de désoxynucléoside triphosphates dans des conditions qui provoquent l'extension de l'amorce, pour ainsi produire l'acide nucléique à deux brins ;
 - (e) répéter les étapes (b) à (d) pour ainsi produire de l'ADN à deux brins (ADN produit) ne contenant que les séquences cibles ;
25
 - (f) cloner l'ADN produit dans des vecteurs d'expression pour l'expression d'un répertoire de protéines dont chacune comprend au moins une partie d'un domaine variable d'immunoglobuline .
30
3. Méthode selon la revendication 2, où les étapes (b) à (d) sont répétées un certain nombre de fois avant l'étape (f).
4. Méthode selon la revendication 1, qui consiste à :
 - (a) produire un répertoire d'ARNm ;
 - (b) recuire, sur l'ARNm, une amorce d'oligonucléotides spécifique d'une séquence à ou adjacente à l'extrémité 3' de chacune des séquences cibles sur les brins de sens, dans des conditions qui permettent à l'amorce de s'hybrider spécifiquement à l'acide nucléique ;
35
 - (c) traiter l'ARNm recuit à l'amorce par une enzyme polymérase en présence de désoxynucléoside triphosphates dans des conditions qui provoquent l'extension de l'amorce pour ainsi produire l'ADNc anti-sens ;
 - (d) recuire, à l'ADNc, une amorce d'oligonucléotides spécifique d'une séquence à ou adjacente à l'extrémité 3' de chacune des séquences cibles sur les brins anti-sens, dans des conditions qui permettent à l'amorce de s'hybrider spécifiquement à l'acide nucléique ;
40
 - (e) traiter l'ADNc recuit à l'amorce par une enzyme polymérase en présence de désoxynucléoside triphosphates dans des conditions qui provoquent l'extension de l'amorce, pour ainsi produire de l'ADN à deux brins (ADN produit) ;
45

(f) cloner l'ADN produit dans des vecteurs d'expression pour l'expression d'un répertoire de protéines, chacune comprenant au moins une partie d'un domaine variable d'immunoglobuline .

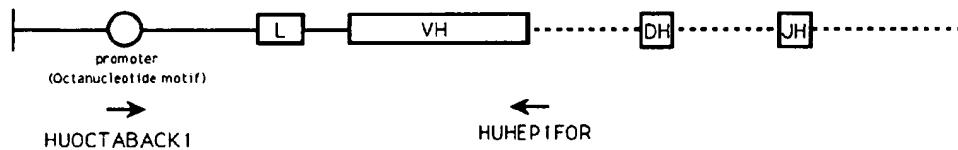
5. Méthode selon la revendication 4 où, après l'étape (e), on accomplit, avant l'étape (f), les étapes suivantes :
 - (i) provoquer la séparation des deux brins de l'ADN produit;
 - (ii) recuire, aux brins séparés, une amorce d'oligonucléotides vers l'avant et vers l'arrière, l'amorce vers l'avant étant spécifique d'une séquence à ou adjacente à l'extrémité 3' du brin de sens de chacune des séquences cibles, l'amorce vers l'arrière étant spécifique d'une séquence à ou adjacente à l'extrémité 3' du brin d'anti-sens de chacune des séquences cibles, dans des conditions qui permettent aux amores de s'hybrider spécifiquement à l'acide nucléique ;
 - (iii) traiter l'échantillon recuit avec une enzyme d'ADN polymérase en présence de désoxynucléoside triphosphates dans des conditions qui provoquent une extension de l'amorce pour ainsi produire l'acide nucléique à deux brins.
15. Méthode selon l'une quelconque des revendications 1 à 5, où l'amorce vers l'arrière est spécifique d'une séquence à ou adjacente à l'extrémité 3' du brin d'anti-sens des séquences qui sont contenues dans les séquences cibles et dont chacune code au moins une partie d'un domaine variable d'immunoglobuline .
20. Méthode selon l'une quelconque des revendications 1 à 6, où le répertoire d'échantillons de l'acide nucléique à deux brins est dérivé de lymphocytes.
25. Méthode selon la revendication 7, où les lymphocytes sont dérivés d'un animal ou humain montrant une réponse immunitaire à un antigène.
30. Méthode selon la revendication 7, où les lymphocytes sont dérivés d'un patient présentant une maladie auto-immune.
35. Méthode selon la revendication 1, où le répertoire d'échantillons de l'acide nucléique est dérivé de gènes de régions variables d'immunoglobuline qui sont réarrangées.
40. Méthode selon la revendication 1, où le répertoire d'échantillons de l'acide nucléique est l'ADN génomique.
45. Méthode selon la revendication 1, où le répertoire d'échantillons de l'acide nucléique est dérivé de gènes de régions variables d'immunoglobuline qui ne sont pas réarrangées.
50. Méthode selon l'une quelconque des revendications 1 à 12, où la séquence cible contient une séquence codant un domaine variable d'une chaîne lourde d'immunoglobuline.
55. Méthode selon la revendication 13, où l'ADN produit est inséré dans un vecteur d'expression pour l'expression de ligands de domaine simple pouvant être sélectionnés par leur affinité de liaison pour l'antigène.
60. Méthode selon la revendication 13, où l'ADN produit est inséré dans un vecteur d'expression pour l'expression des anticorps ou des fragments d'anticorps pouvant être sélectionnés par leur affinité de liaison pour l'antigène.
65. Méthode selon l'une quelconque des revendications 1 à 13, où l'ADN produit est inséré dans un vecteur d'expression pour l'expression seule.
70. Méthode selon l'une quelconque des revendications 1 à 13, où l'ADN produit est inséré dans un vecteur d'expression pour l'expression en combinaison avec un domaine variable complémentaire.
75. Méthode selon l'une quelconque des revendications 1 à 13, où l'ADN produit est inséré dans un vecteur d'expression contenant déjà des séquences codant un ou plusieurs domaines constants pour l'expression.

19. Méthode selon l'une quelconque des revendications 1 à 13, où l'ADN produit est inséré dans un vecteur d'expression pour l'expression en tant que protéines de fusion.
- 5 20. Méthode selon l'une quelconque des revendications 1 à 13, où l'ADN produit est inséré dans un vecteur d'expression pour l'expression avec des marqueurs de peptides.
- 10 21. Méthode selon l'une quelconque des revendications 1 à 13, où l'ADN produit contenant des séquences codant au moins des domaines variables de chaîne lourde d'immunoglobuline et l'ADN produit contenant des séquences codant au moins des domaines variables de chaîne légère d'immunoglobuline sont insérés dans des vecteurs d'expression pour l'expression d'un répertoire en combinaison de domaines variables complémentaires.
- 15 22. Méthode selon la revendication 21, où l'ADN produit est inséré dans un vecteur d'expression contenant déjà des séquences codant un ou plusieurs domaines constants pour l'expression.
23. Méthode selon la revendication 21, où l'ADN produit est inséré dans des vecteurs d'expression pour l'expression en tant que protéines de fusion.
- 20 24. Méthode selon la revendication 21, où l'ADN produit est inséré dans un vecteur d'expression pour l'expression avec des marqueurs de peptides.
- 25 25. Méthode selon l'une quelconque des revendications 1 à 24, où les amorces vers l'avant et vers l'arrière sont produites sous la forme d'oligonucléotides simples.
26. Méthode selon l'une quelconque des revendications 1 à 24, où les amorces vers l'avant sont fournies sous la forme d'un mélange d'oligonucléotides.
- 30 27. Méthode selon l'une quelconque des revendications 1 à 24, où les amorces vers l'arrière sont fournies sous la forme d'un mélange d'oligonucléotides.
28. Méthode selon l'une quelconque des revendications 1 à 27, où chaque amorce contient une séquence codant un site de reconnaissance d'une enzyme de restriction.
- 35 29. Méthode selon la revendication 28, où le site de reconnaissance d'une enzyme de restriction est placé dans la séquence qui est recuite à l'acide nucléique.
- 30 30. Méthode selon la revendication 1, où l'amorce vers l'arrière est une amorce générale utile pour cloner une spécificité d'anticorps souhaité d'une espèce spécifique.
- 40 31. Méthode selon la revendication 1, où l'amorce vers l'arrière est un mélange d'amorces ayant une variété de séquences désignées pour être complémentaires aux diverses familles des séquences VH, Vk ou V.
- 45 32. Librairie d'expression comprenant un répertoire de séquences d'acides nucléiques dont chacune code au moins une partie d'un domaine variable d'immunoglobuline.

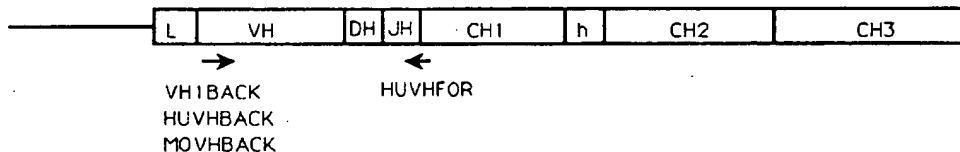
Rearranged heavy chain variable gene (DNA)



Unrearranged heavy chain variable gene (DNA)



Rearranged heavy chain variable gene (mRNA)



Rearranged light chain variable gene (DNA)

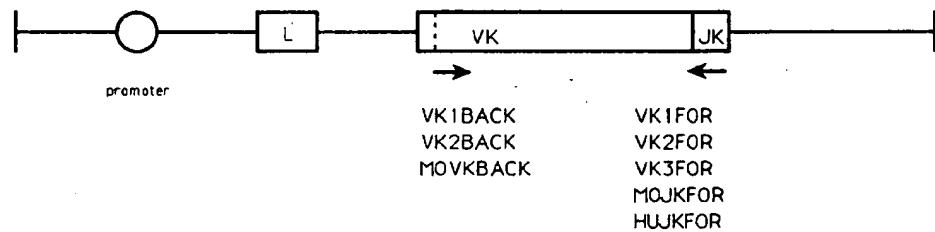


FIG. 1

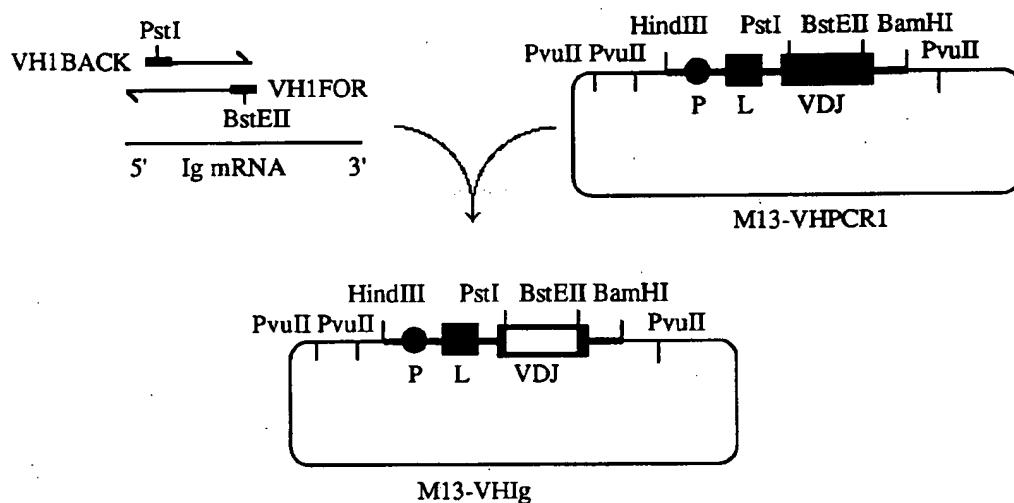


FIG. 2

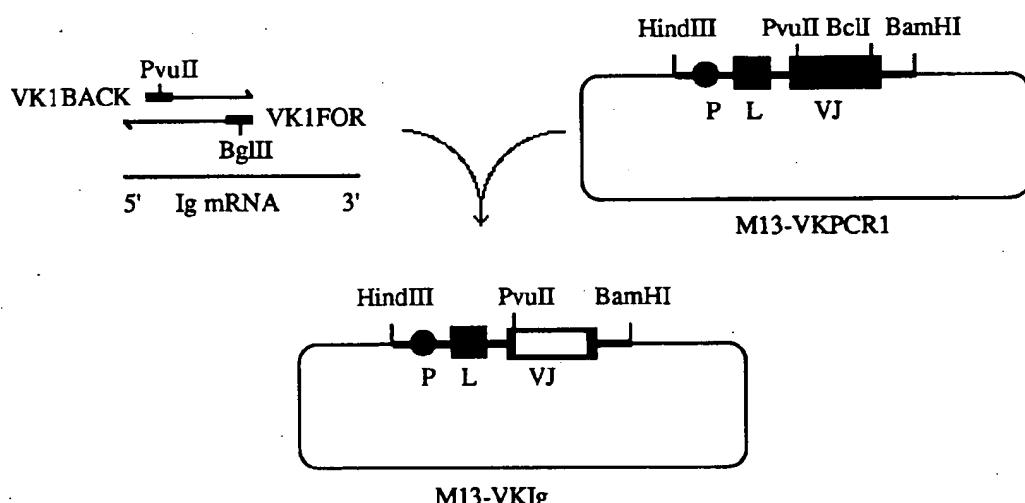


FIG. 4

M13 VHPCR1.HinD III⁽¹⁾

AAGCTTATGAATATGCAAATCCTCTGAATCTACATGGTAAATATAGGTTGTCTATACCA
 10 20 30 40 50 60
 CAAACAGAAAAACATGAGATCACAGTTCTCTACAGTTACTGAGCACACAGGACCTCAC
 70 80 90 100 110 120

M G W S C I I L F L V A T A T
 CATGGGATGGAGCTGTATCATCCTCTTGGTAGCAACAGCTACAGGTAAAGGGCTCAC
 130 140 150 160 170 180

AGTAGCAGGCTTGAGGTCTGGACATATATATGGGTGACAATGACATCCACTTCGCCTTC
 190 200 210 220 230 240

PstI
 1 51 10
 G V H S Q V Q L Q E S G P G L V R P
 TCTCCACAGGTGCCACTCCCAGGTCCAACCTGGAGGAGCGGTCCAGGTCTGTGAGAC
 250 260 270 280 290 300

CDR1
 15 20 25 30
 S Q T L S L T C T V S G S T F S S Y W M
 CTAGCCAGACCTTGAGCTGACCTGCACCGTGTCTGGCAGCACCTTCAGCAGCTACTGGA
 310 320 330 340 350 360

CDR2
 35 40 45 50
 H W V R Q P P G R G L E W I G R I D P N
 TGCACTGGGTGAGACAGCCACCTGGACGAGGTCTGGAGTGGATTGAAAGGATTGATCCTA
 370 380 390 400 410 420

55 60 65 70
 S G G T K Y N E K F K S R V T M L V D T
 ATAGTGGTGGTACTAACATGAGAAGTCAAGAGCAGAGTGACAATGCTGGTAGACA
 430 440 450 460 470 480

75 80 85 90
 S K N Q F S L R L S S V T A A D T A V Y
 CCAGCAAGAACAGTTCAACCTGGAGACTCAGCAGCGTGACAGCCGCCACACCGCGGTCT
 490 500 510 520 530 540

CDR3
 95 100 105 110
 Y C A R Y D Y Y G S S Y F D Y W G Q G T
 ATTATTGTGCAAGATAACGATTACTACGGTAGTAGCTACTTGTACTGGGCCAAGGGA
 550 560 570 580 590 600

BstEII
 115 120
 T V T V S S
 CCACGGTCACCGTCTCTCAGGTGAGTCCTTACAACCTCTCTCTATTCAAGCTAAAT
 610 620 630 640 650 660

AGATTTTACTGCATTGTTGGGGGGAAATGTGTGTATCTGAATTTCAGGTCAATGAGGA
 670 680 690 700 710 720

CTAGGGACACCTTGGGAGTCAGAAAGGTCATTGGGAGCCCCGGCTGATCCAGACAGACA
 730 740 750 760 770 780

BamHI

790 800 810

FIG. 3

M13 VK-PCR1

Hind III

AAGCTTATGAAATATGCAAATCCTCTGAATCTACATGGTAAATAGGTTGTCTATACCA
 38 48 58 68 78 88

CAAACAGAAAAACATGAGATCACAGTTCTCTACAGTTACTGAGCACACAGGACCTCAC
 98 108 118 128 138 148

M G W S C I I L F L V A T A T
 CATGGGATGGAGCTGTATCATCCTCTTGGTAGAACAGCTACAGTAAGGGCTCAC
 158 168 178 188 198 208

AGTAGGCAGGCTTGAGGTCTGGACATATATGGGTGACAATGACATCCACTTGCCTTC
 218 228 238 248 258 268

Pvu II

G V H S D I Q L T Q S P S S L S A S
 1 5 10
 TCTCCACAGGTGTCCACTCCGACATOCAGCTGACCCAGAGCCAAAGCAGCCTGAGGCCA
 278 288 298 308 318 328

CDR1

15 20 25 30
 V G D R V T I T C R A S G N I H N Y L A
 CGCTGGGTGACAGAGTGACCATCACCTGTAGAGCCAGCGTAACATCCACAACTACCTGG
 338 348 358 368 378 388

CDR2

35 40 45 50
 W Y Q Q K P G K A P K L L I Y Y T T T L
 CTTGGTACCAAGCAGAACGCCAGGTAAGGCTCCAAAGCTGCTGATCTACTACACCACCC
 398 408 418 428 438 448

55 60 65 70
 A D G V P S R F S G S G S G T D F T F T
 TGGCTGACGGTGTGCCAACGAGATTCAAGCGTAGCGGTAGCGGTACCGACTTCACCTTCA
 458 468 478 488 498 508

CDR3

75 80 85 90
 I S S L Q P E D I A T Y Y C Q H F W S T
 CCATCAGCAGCTCCAGCCAGAGGACATGCCACCTACTACTGCCAGCACTCTGGAGCA
 518 528 538 548 558 568

Bcl I (requires dam⁻ host)

95 100 105 108
 P R T F G Q G T K V V I K R
 CCCCCAAGGACGTTGGCCAAGGGACCAAGGTGGTGATCAAACGTGAGTAGAATTAAACT
 578 588 598 608 618 628

BamHI

TTGCTTCCTCAGTTGGATCC
 638 648

FIG. 5

Sequence of MBr1 VH

Splice -1
↓ G V H S
AGGTGTCCACTCC

1 PstI	10	20
Q V Q L O E S G T E L A S P G A S V T L		
<u>CAGGTCCAAC</u> TGCA <u>GAGGACTCAGGA</u> ACTGAGCTGGCAGTCCTGGGCATCAGTGACACTG		
VH1BACK SITE		
30 CDR1	40	52a 53 CDR2
S C K A S G Y T F T D H I I N W V K K R		
TCCTGCAAGGCTTCTGGCTACACATTACTGACCATAATTGGTAAGGGAAAAAGAGG		
P G Q G L E W I G R I Y P V S G V T N Y		
CCTGGACAGGGCCTTGAGTGATTGGAAAGGATTATCCAGTAAGTGGTGAACTAAC		
60 CDR2 65 70 CDR3		
N O K F M G K A T F S V D R S S N T V Y		
AATCAAAAATTATGGCAAGGCCACATTCTCTGTAGACCGGTCTCCAACACAGTGTAC		
80 82A B C 83 90 CDR3		
M V L N S L T S E D P A V Y Y C G R G E		
ATGGTGGTGAACAGTCTGACATCTGAGGACCCCTGCTGTCTATTACTGTGGAAGGGGCTT		
CDR3 103 BstEII Splice		
D F D Y W G Q G T T V T V S S ↓		
GATTTGACTACT <u>GGGCAAGGGACCA</u> CGGTCTACCGTCTCAGGT.....		
VH1FOR SITE		

Sequence of MBr1 VK

Splice -1
↓ G V H S
AGGTGTCCACTCC

1 PvuII	10	20
D I Q L T Q S P P S L T V S V G E R V T		
<u>GACATTCA</u> GCTGACCCAGTCTCCACCATCCCTGACTGTGTCA <u>G</u> TAGGAGAGGGTCACT		
VK1BACK SITE		
27A B C D E F CDR1		
I S C K S N O N L L W S G N R R Y C L G		
ATCA <u>GGT</u> CAAAT <u>CCAA</u> TCAGAA <u>CTTT</u> TATGG <u>ACT</u> GGAA <u>ACCG</u> AAGGTACTGTTGGGC		
35 40 50 CDR2		
W H Q W K P G Q T P T P L I T W T S D R		
TGGCAC <u>CA</u> GTGGAA <u>AC</u> GGCAAA <u>CT</u> CACACCGTGT <u>AC</u> CC <u>GT</u> GATCAC <u>CT</u> GGACAT <u>CT</u> GATAGG		
60 70 CDR3		
F S G V P D R F I G S G S V T D F T L T		
TTCTCTGGAGTCCC <u>GT</u> AT <u>GT</u> CT <u>GT</u> TCATAG <u>GG</u> <u>AG</u> <u>GT</u> GG <u>CA</u> <u>GT</u> TT <u>AT</u> TT <u>CT</u> GT <u>CA</u> <u>GC</u> <u>AA</u> <u>CA</u> <u>CT</u> GG <u>AC</u> <u>CT</u> TT		
80 90 CDR3		
I S S V Q A E D V A V Y F C Q Q H L D L		
ATCAG <u>GG</u> <u>AG</u> <u>GT</u> GC <u>AG</u> <u>GT</u> GA <u>AG</u> <u>AT</u> GT <u>GG</u> <u>CA</u> <u>GT</u> TT <u>AT</u> TT <u>CT</u> GT <u>CA</u> <u>GC</u> <u>AA</u> <u>CA</u> <u>CT</u> GG <u>AC</u> <u>CT</u> TT		
95 100 BglII/BclI Splice		
P Y T F G G G T K L E I K ↓		
CCGTACAC <u>GT</u> TC <u>GG</u> <u>AG</u> <u>GG</u> <u>AC</u> <u>CA</u> <u>AG</u> <u>GT</u> GG <u>AG</u> <u>AT</u> CA <u>AA</u> <u>AC</u> <u>GT</u> GAG		
VK1FOR SITE		

FIG. 6

α -Lys 30

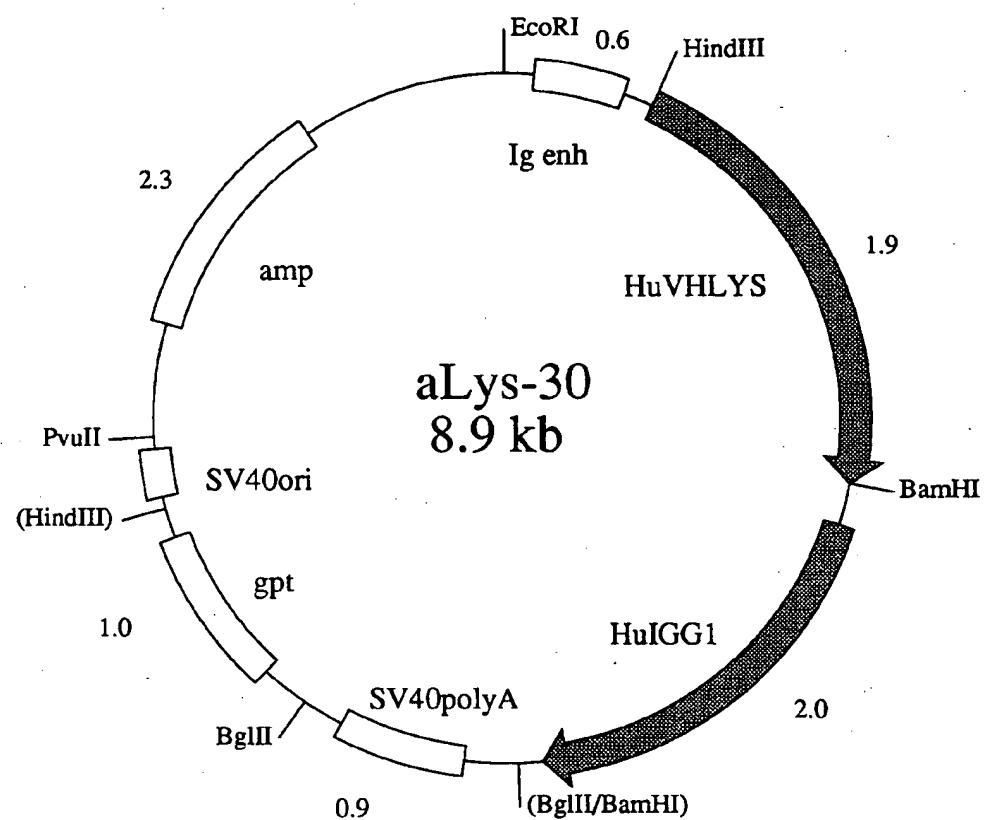


FIG. 7

α -Lys 17

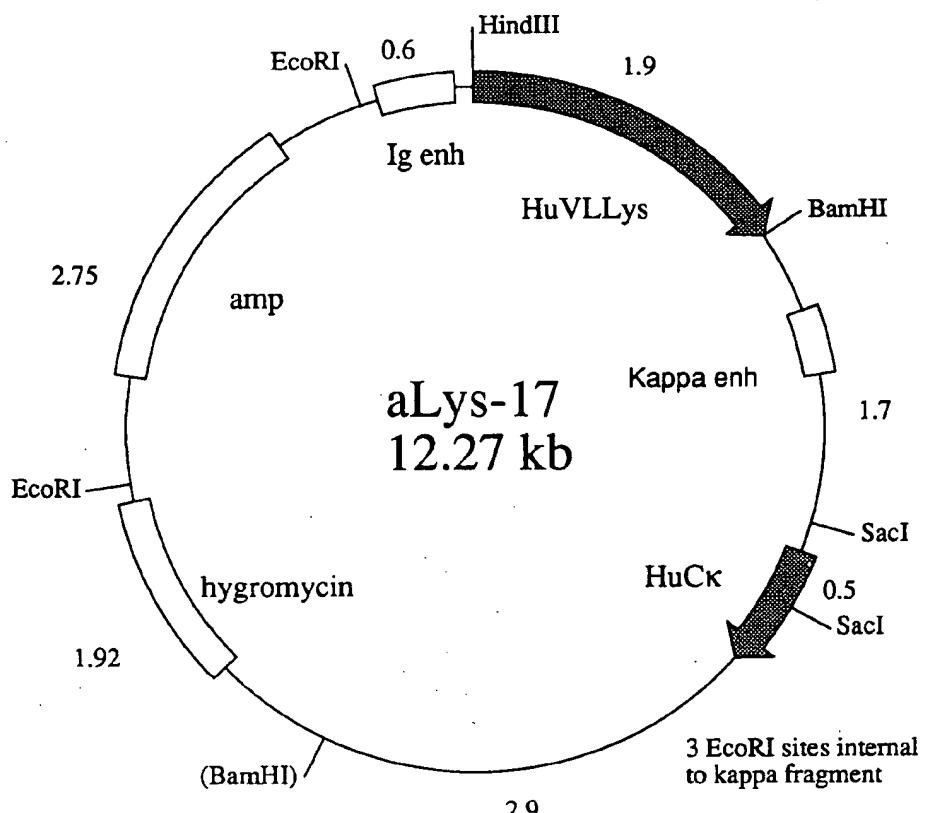


FIG. 8

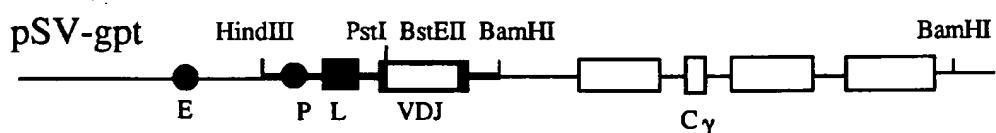
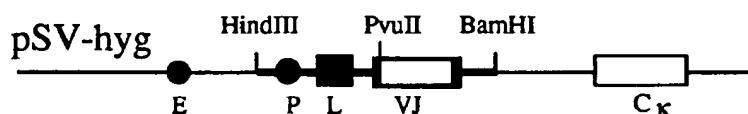


FIG. 9



	ER1	CDR_1	ER2	CDR_2
KABAT IA				
A07	PGLVKPSQSLSLTCSVTGYSIT	SGYYWN	WIRQFPGNKLEWMG	YISYDGSNNYNPSLKN
A09	PGLVKPSQSLFLTCISITGFPI	SGYYWI	WIRQSPGKPLEWMG	YITHSGETFYNPSLQS
E03	PGLVKPSQSLSLTCSVTGYSIT	SGYYWN	WIRQFPGNKLEWMG	YISYDGSNNYNPSLKN
G01	PGLVKPSQSLSLTCSVTGYSIT	SGYYWN	WIRQFPGNKLEWMG	YISYDGSNNYNPSLKN
KABAT IB				
A06	PVLVAPSQSLSITCAVSDFSLT	NYGVL	WVRQPPGKGLEWLIG	VIWAGGITNYNSALMS
25G07	PGLVQPSQSLSITCTVSGFSLT	SYGVH	WVRQSPGKGLEWLIG	VIWSGGSTDYNAAFIS
B03	PGLVAPSQSLSITCTVSGFSLT	SYGVD	WVRQPPGKGLEWLIG	VIWGGGSTNYNSALMS
G03	PGLVQPSQSLSITCTVSGFSLT	SYGVH	WVRQSPGKGLEWLIG	VIWSGGSTDYNAAFIS
H09	PVLVAPSQSLSITCTVSGFSLT	SYGVH	WVRQPPGKGLEWLIG	VIWAGGSTNYNSALMS
25C10	PGLVAPSQSLSITCTVSGFSLT	SYAIS	WVRQPPGKGLEWLIG	VIWTGGGTNYNSALKS
A12	PGLVAPSQSLSITCTVSGFSLT	SYAIS	WVRQPPGKGLEWLIG	VIWTGGGTNYNSALKS
A08	PGLVAPSQSLSITCTVSGFSLT	SYGVH	WVRQPPGKGLEWLIG**	*** * * * GSTITNSALKS
25G08	PGLVAPSQSLSITCTVSGFSLT	SYDVD	WVRQSPGKGLEWLIG	VIWGGGSTNYNSALKS
A03	PGLVAPSQSLSITCTVSGFSLT	SYGVH	WVRQSPGKGLEWLIG	VIWSGGSTDYNAAFIS
C07	PVLVAPSQSLSITCTVSGFSLT	SYGVH	WVRQPPGKGLEWLIG	VIWAGGSTNYNSALMS
H04	PGLVAPSQSLSITCTVSGFSLT	SYGVD	WVRQSPGKGLEWLIG	VIWVGSTNYNSALKS
KABAT IIA				
E04	PELVRPGSVKISCKGSGYFTFT	DYAMH	WVKQSHAKSLEWIG	VISTYYGDASYNQFKD
H07	PELVRPGSVKISCKGSGYFTFT	DYAMH	WVKQSHAKSLEWIG	VISTYYGDASYNQFKD
KABAT IIB				
A02	AELVMPGASV р KLSCKASGYFTFT	SYWMH	WVKQRPQGQGLEWIG	EIDPSDSYTNYNQFKG
B04	AELVKPGASV р KMSCKASGYFTFT	SYWIT	WVKQRPQGQGLEWIG	DIYPGSGSTNYNEKFKS
C05	AELVKPGASV р KLSCKASGYFTFT	SYNMH	WVKQRPGRGLEWIG	RIDPNSGGTKYNEKFKS
C09	AELVKPGASV р KLSCKASGYFTFT	SYNMH	WVKQRPQGQGLEWIG	EINPSNGGTNYDEKFKS
D06	ASLVKPGASV р KMSCKASGYFTFT	SYWIT	WVKQRPQGQGLEWIG	DIYPGSGSTNYNEKFKS
D08	PELVKPGASV р KLSCKASGYFTFT	SYNMH	WVKQRPQGQGLEWIG	EINPSNGGTNYNEKFKS
E07	AELVMPGASV р KLSCKASGYFTFT	DYEMH	WVKQTPVHGLEWIG	AIDPETCGTAYNQFKG
G08	PELVKPGASV р KLSCKASGYFTFT	DYYIN	WVKQRPQGQGLEWIG	WIYPGSGNTKYNEKFKG
G10	AELVMPGASV р KMSCKASGYFTFT	SYWMH	WVKQRPQGQGLEWIG	RIMPSDSDTNYNQFKG
25G09	AELVMPGASV р KMSCKASGYFTFT	TYPIE	WVKQNRHKSLLEWIG	NFHPYNDDTKYNEKFKG
F04	TELVKPGASV р KLSCKASGYFTFT	SYWMH	WVKQRPQGQGLEWIG	NINPSNGGTNYNQFKG
H02	AELVMPGASV р KLSCKASGYFTFT	SYWMH	WVKQRPQGQGLEWIG	NIDPSDSETHYNQFKD
H01	AELVMPGASV р KLSCKASGYFTFT	SYWMH	WVKQRPQGQGLEWIG	EIDPSDSYTNYN * KVQG
25C05	PELVRPGTSV р KMSCKASGYFTFT	NYWMK	WV * ORPQGQGLEWIG	QIPFASGSIYVNEHDK
B01	AELVKPGASV р KMSCKASGYFTFT	SYWIT	WVKQRPQGQGLEWIG	DIYPGSGSTNYNEKFKS
B05	AELVRPGSSV р KLSCKDSYFAFM	RHAMH	WVKQRPQGQGLEWIG	SFTMYSDATEYSENFKG
B11	AELVKPGASV р KMSCKASGYFTFT	SYWIT	WVKQRPQGQGLEWIG	DIYPGSGSTNYNEKFKS
KABAT III A				
25G05	GGLVQAWSLSLSCAASGFTFT	DYYMS	WVRQPPGKALEWLIG	FIRNKANGYTTESASVKG
C10	GGLVQPGGSLSLSCAASGFTFT	DYYMN	WVRQPPGKALEWLA	LIRHKANGYTMYESASVKG
B07	GGLVQPGGSLSLSCAASGFTFT	DYYMS	WVRQPPGKALEWLA	LIRNKANGYTTESASVKG
KABAT III B				
G05	GGLVPGGSLKLSCAASGFTFS	DYGMH	WVRQAPEKGLEWVA	YISSGSSSTIYYADTVKG
B12	GGLVQPGESLKLSCESNEYEFFP	SHDMS	WVR*****VA	AINSDGGSTYYPDIMER
D04	GGLVQPGGSLRLSCAASGFTFS	SYAMS	WVA * APGKGLEWVS	AISGSGGSTYYADSVKG
D05	GGLVQPGGSLRLSCAASGFTFS	SYAMS	WVA * APGKGLEWVS	AISGSGGSTYYADSVKG
F12	GGLVQPGESWKLSCLCVIO****	*****	WVRQ*PKRLELVA	AINSDGGSTYYPDIMER
F06	GGLVQPGGSLRLSCAASGFTFS	SYAMS	WVA * APGKGLEWVS	AISGSGGSTYYADSAKG
D02	GGLVQPGESLKLSCESNEYVIP	*HDMS	WVRQDSGE * LELVA	AINSDGGSTYYPDIMER
F09	GDLVKPGGSLKLSCAASGFTFS	SYGMS	WVRQTPDKRLEWVA	TISSGGSYTYYPDSDKVKG
KABAT III C				
E06	GGLVQPGGSMKLSCAASGFTFS	DAWMD	WVRQSPEKGLEWVA	EIRNKANNHATYYAESVKG
KABAT V A				
C04	AELVKPGASV р KLSCKASGYFTFT	EYTIH	WVKQRSGQGLEWIG	WFYPGSGSIKYNEKFKD

FIG. 10a

FR 3CDR 3

RISITRDTSKNQFFLKLNSVTTEDTATYYCAR PISITRETSKNQFFLQLNSVTTEDTAMYYCAG RISITRDTSKNQFFLQLNSVTTEDTATYYCAR RISITRDTSKNQFFLKLNSVTTEDTATYYCAR	EGNWDFGAY DRDKLGPWFAY DSSGSMDY VSSGYESMDY
RLSISKDTSKSVFVLKMSLQTDDTAVYYCAK RLSISKDN SKSQVFFKMSLQADDTAIYYCAR RLSISKDN SKSQVFLKMSLQTDDTAMYYCAK RLSISKDN SKSQVFFKMSLQADDTAIYYCAR RLSISKDN SKSQVFLKMSLQTDDTAMYYCAI RLSISKDN SKSQVFLKMSLQTDDTARYYYCAR RLSISKDN SKSQVFLKMSLQTDDTARYYYCAR RLSISKDN SKSQVFLKMSLQTDDTAMYYCAR RLSISKDN SKSQVFLKMSLQTDDTAMYYCAR RLSISKDN SKSQVFLKMSLQTDDTAMYYCAK RLSISKDN SKSQVFLKMSLQTDDTAMYYCAS	HGDSSGYFDY NDGYY LGRGYAMDY KRDYDYDRGYYYAMDY YYDGSSPFAY EGYYYFAY IYYDGSSDYYAMDY 13 nt. Ps.gene/Unproductive 21 nt. Unproductive 28 nt. Unproductive 37 nt. Unproductive 32 nt. Unproductive
KATMTVDKSSSTAYMELARLTSEDSAVYYCAR KATMTVDKSSSTAYMELARLTSEDSAVYYCAR	40 nt. Unproductive 22 nt. Unproductive
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCVR KATLTVDTSSTAYMQLSSLTSEDSAVYYCAR KATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR KATLTVDKSSSTAYMQLSSLTSEDSAVYYCTL KATLTVDTSSTAYMQLSSLTSEDSAVYYCAR KATLTVDKSSSTAYMQLSSLTSEDSAVYYCTI KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR KATLTVDTSSTAYMQLSSLTSEDSAVYYCAR KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAI KATLTVEKSSSTVYLELSRLTSEDSAVYYCAR KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAP KAANAVDTSSSTAYMQLSSLTSEDTAVYYFCL* KATLTVDKPSDTAYMQLSSLTSEDSASYYCAR KATLTANTSSSTAYMELSSLTSEDSAVYYCAR KATLTVDTSSTS YMQLSSLTSEDSAVYYCAR	RGLTYAMDY YYSNYFDY PNWDHYYYGMDV LYYYAMDY SSGYDY GAARATNAY GGFAY SPMDY EVPGGFYATDY MDYGYSSLWFAY TTVVAFDY KRDYSTYFDH TGTEFAY 24 nt. Ps.gene 9 nt. Ps.gene/Unproductive 23 nt. Unproductive 15 nt. Unproductive
RFTISRDNSQSILYLQMNALRAEDSATYYCAR RFTISRDNSQSILYLQMNALRAEDSATYYCAR RFTISRDNSQSILYLQMNALRAEDSATYYCAR	YMLLGAMDY GYYDGSSYYAMDY 23 nt. Unproductive
RFTISRDNAKNTLFLQMISLRSEDTAMYYCAR RFIIISRDNTKKTLYLQMSSLRSEDTALLYCAR RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAD RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK RFIIISRDNSKKTLYLQMSSLRSEDTALLYCAR RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR RFIIISRDNTKKTLYLQMSSLRSEDTALLYCAR RFTISRDNAKNTLYLQMSSLKSEDTAMYYCAR	AKFHLYFDY REGVVESRLDGDV RGLHWFDP RNYGSSPFDY PPMPSY 43 nt. Ps.gene 28 nt. Ps.gene 35 nt. Ps.gene/Unproductive Ps.gene/Unproductive Unproductive
RFTISRDDSKSRVYLQMNSLRAEDTGIYYCTG	30 nt. Unproductive

KATLTADKSSSTVYMELSLRTSEDSAVYFCAR HEDRDSSGYAMDY

FIG. 10 b

CDR 2FRAMWORK 3CDR 3

KABAT HUMAN VH1

HAQKFQG	STSTAYMELRSLRSEDTAVYYCAR	GEGWDHFDY
GYAQKFQG	RVTIRRHKSTSTAYMELSSLRSEDTAVYYCAR	GSRYGYDCSGYYYL
	RVTMTRNTSISTATMELSSLRSEDTAVYYCAR	LAHFSGSPVDFD

KABAT HUMAN VH2

KHQLQPSLKS	RVTISVDTSKNQFSKLSSVTAADTAVYYCAR	GGVVPAAIMDV
KS	RVTISVDTSKNQFSKLSSVTAADTAVYYCAR	MARYYDFWSGYSAYYDY
SLKS	RLSISQDTSRNQFSLRLLSSVTAADTAVYYCAR	HRNWGPSVHFDF
	ESTSTAYMELSSLRSEDTAVYYCAR	DSYGDYGGHY

KABAT HUMAN VH3

ISYITSSSYTYADSVKG	RFTISRDNAKNSLYLQMNSLRADDTAVYYCAR	DGRFGTYSPSDY
SVKG	RFTISRDDSKSIAYLQVNLSLKTEDTAVYYCTR	TIYYDSSGYPW
YADSVKG	RFTISRDNAKNSLFQMQSSLRAEDTAFYCAR	GIALDAFDI
YYADSVRD	RFTISRDNSKNTLYLQMNSLRRAEDTAVYYCAK	53 NT. UNPROD REARR
DSVKG	RFTISRDNAKNSLYLQMNSLRDEDTAVYYCAR	DHSCTGGGSGSYF
VSATSGGGSTYYADSVKG	RFTISRDNPKNTLYLQMNSLRSEDTAVYYCAR	KDNLWFDP
AVISYDGSNKYADSVKG	RFTISRDNSKNTLYLQMNSLRRAEDTAVYYCAR	DLGGRGVVVVPAPGGRSITYYGMDV
GAVISYDGSNKYADSVKG	RFTISRDNSKNTLYLQMNSLRRAEDTAVYYCAS	LEGIGTIYYYGMDV
	AKNSLYLQMNSLRRAEDTAVYYCVR	DDSSSWPKHFQH
QYAASVKG	RFTISRDDSKNSLYLQMNSLNTEDTAVYYCVR	SGVVPYLDY

KNOWN FAMILY

AVYYCAR	DPRIAARPDDYYYYMDV
TAMYYCAR	GAEVVEPTARYYYGLNV

FIG. 11

FR1	CDR1	FR2
Y TFT	SY GIS	W VTTGPWTRDLRWMG
GEKPGSSVKVSCKASGY TFT	DY FMN	W MRQAPGQRLEWMG
QVQLQEIGPRTGEASET LSLICAVSGDSIS	SG NW*I	W VRQPPGKGLEWIG
QVQLQESGPGLVK*SETLSLTCTVSGGSIS	S Y WS	W IrqppGKGLEWIG
GY TFT	NY CMH	W VRQDHQAQGLEWMG
QVQLQESGPGLVKpSETLSLYCAVSGDSIS	SG NW*I	W VRQPPGKGLEWIG
GP RLGEASET LSLICAVSGDSIS	SS SYY W	W IRQPPGKGLEWIG
QVQLQESGPGLVKpSETLSLTCTVSGGSIS	S Y WS	W IRQPPGKGLEWIG
LSLICAVSGSSIS	SG NW*I	W VRQPPGKGLEWIG
SETLSLTCAVYGGFS	G YY WS	W IRQPPGKGLEWIG
QVQLVQSGAEVKKPGSSVKVSCKASGY TFT	NY CMH	W VRQVLAQGLEWMG
SETLSLICAVSGDSIS	SG NW*I	W VRQPPGKGLEWIG
SRAQTGEASET LSLICAVSGDSIS	SS SYY WG	W IRQPPGKGLEWIG
CPLTC TVSGSVSSGS	YY WS	W IRQPPGKGLEWIG
GLVKPSETLSLTCTVSGGSIS	S Y WS	W IGS PpGKGLEWIG
SFETLSLICAVSGDSIS	SG NW*I	W VRQPPGKGLEWIG
QVQLVQSGAEVKKPGSSVKVSCKASGGTFS	SY AIS	W VRQAPGQGLEWMG
QVQLQQWGA GLLKPS ETLSLTCAVYGGFS	G YY WS	W IRQPPGKGLEWIG
QIQLQESGPGLVKPSETLSLTCTVSGGSIS	SS SYY WG	W IRQPPGKGLEWIG
GP GLVKPQS TLSLTCTVSGGSIS	SG G YY WS	W IRQNP GKGLEWIG

* indicates stop codon (unsure as sequence remains in frame)
 • sequence terminates due to internal restriction site
 lower case denotes frame shift

CDR2	FR3	CDR3
W ISAYNGNT NYAQKLOG	R VTMTDTST STAYMELRSLRSDDT AVYY CAR	DTVSS
WINAGNGNT KYSQKLOG	R VTITRDTS A STAYMQLSSLRSE DT AVYY CAR	DTVSS
EIHHSGSTYYNPSLKS	R ITMSV DTSK NQFY LKLSS•	
RIY TSGST NYNPSLKS	R VTISV DTSK NQFS LKLSS VTAA DT AVYY CAR	DTVSS
LVCPSDGSTS YAQKFQA	R VTITRDTS M STAYMELSSLRSE DT AM YY CAR	DTVSS
EIHHSGSTYYNPSLKS	R ITMSV DTSK NQFY LKLSS•	
EINHSGST NYNPSLKS	R VTISV DTSK NQFS LKLSS•	
YIY SGST NYNPSLKS	R VTISV DTSK NQFS LKLSS•	
EIHHSGSTYYNPSLKS	R ITMSV DTSK NQFY LKLSS•	
EINHSGST NYNPSLKS	R VTISV DTSK NQFS LKLSS VTAA DT AVYY CAR	DTVSS
LVCPSDGSTS YAQKFQA	R VTITRDTS M STAYMELSSLRSE DT AM YY CAR	DTVSS
EIHHSGSTYYNPSLKS	R ITMSV DTSK NQFY LKLSS•	
SIY SGST YYNPSLKS	R VTIPV DTSK NQFS LKLSS•	
YIY SGST NYNPSLKS	R VTISV DTSK NQFS LKLSS VTAA DT AVYY CAR	DTVSS
RIY TSGST NYNPSLKS	R VTMSV DTSK NQFS LKLSS•	
EIHHSGSTYYNPSLKS	R ITMSV DTSK NQFY LKLSS•	
RIIPILGIAN YAQKFQG	R VTITADKST STAYMELSSLRSE DT AVYY CAR	DTVS
EINHSGST NYNPSLKS	R VTISV DTSK NQFS LKLSS•	
EINHSGST NYNPSLKS	R VTISV DTSK NQFS LKLSS•	
YIY SGST YYNPSLKS	R VTISV DTSK NQFS LKLSS VTAA DT AVYY CAR	DTVSS

FIG. 12

pSW1

HindIII site AAGCTT

	M	K	Y	L	L	P	T	A	A
GCATGCAAATTCTATTCAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC									
10	20	30	40	50	60				

A	G	L	L	L	A	A	Q	P	A	M	A	Q	V	Q	L	Q	E	S
GCTGGATTGTTATTACTCGCTGCCAACCCAGCGATGGCCAGGTGCAGCTGCAGGAGTC																		
70	80	90	100	110	120													

G	P	G	L	V	A	P	S	Q	S	L	S	I	T	C	T	T	V	S	G	F
GGACCTGGCCTGGTGGCGCCCTCACAGCCTGTCATCACATGCACCGTCTCAGGGTTC																				
130	140	150	160	170	180															

S	L	T	G	Y	G	V	N	W	V	R	Q	P	P	G	K	G	L	E	W
TCATTAACCGGCTATGGTGTAAACTGGGTCGCCAGCCTCCACGAAAGGTCTGGAGTGG																			
190	200	210	220	230	240														

L	G	M	I	W	G	D	G	N	T	D	Y	N	S	A	L	K	S	R	L
CTGGGAATGATTGGGTGATGAAACAGACTATAATTAGCTCTCAAATCCAGACTG																			
250	260	270	280	290	300														

S	I	S	K	D	N	S	K	S	Q	V	F	L	K	M	N	S	L	H	T
AGCATCAGCAAGGACAACCTCAAGAGCCAAGTTCTAAAAATGAACAGTCTGCACACT																			
310	320	330	340	350	360														

D	D	T	A	R	Y	Y	C	A	R	E	R	D	Y	R	L	D	Y	W	G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTACTGGGC																			
370	380	390	400	410	420														

Q	G	T	T	V	T	V	S	S												
CAAGGCACCAACGGTCACCGTCTCCTCATAATAAGAGCTATCCCAGGCTAAGCTCGAATT																				
430	440	450	460	470	480															

FIG. 13

pSW2

HindIII AAGCTT

		M	K	Y	L	L	P	T	A	A
GCATGCAAATTCTATTCAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC										
10	20	30	40	50	60					
A G L L L L A A Q P A M A Q V Q L Q E S										
GCTGGATTGTTATTACTCGCTGCCAACAGCGATGGCCAGGTGCAGCTGCAGGAGTCA										
70	80	90	100	110	120					
G P G L V A P S Q S L S I T C T V S G F										
GGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCATCACATGCACCGCTCAGGGTTC										
130	140	150	160	170	180					
S L T G Y G V N W V R Q P P G K G L E W										
TCATTAACCGCTATGGTGTAAACTGGGTCGCCAGCCTCAGGAAAGGGTCTGGAGTGG										
190	200	210	220	230	240					
L G M I W G D G N T D Y N S A L K S R L										
CTGGGAATGATTGGGTGATGAAACACAGACTATAATTAGCTCTCAAATCCAGACTG										
250	260	270	280	290	300					
S I S K D N S K S Q V F L K M N S L H T										
AGCATCAGCAAGGACAACCCAAGAGCCAAGTTCTAAAAATGAACAGTCTGCACACT										
310	320	330	340	350	360					
D D T A R Y Y C A R E R D Y R L D Y W G										
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTACTGGGC										
370	380	390	400	410	420					
Q G T T V T V S S										
CAAGGCACACGGTCACCGTCTCCTCATATAAGAGCTGAATTGCCAGCTGCATGC										
430	440	450	460	470	480					
M K Y L L P T A A A G										
AAATTCTATTCAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCTGGA										
490	500	510	520	530	540					
L L L L A A Q P A M A D I V L T Q S P A										
TTGTTATTACTCGCTGCCAACAGCGATGGCGACATCGCTGACTCAGTCTCCAGCC										
550	560	570	580	590	600					
S L S A S V G E T V T I T C R A S G N I										
TCCCTTCTGCGTCTGGAGAAAAGTCACCATCACATGTCGAGCAAGTGGAAATT										
610	620	630	640	650	660					
H N Y L A W Y Q Q K Q G K S P Q L L V Y										
CACAATTATTTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTAT										
670	680	690	700	710	720					

FIG. 14a

Y T T T L A D G V P S R F S G S G S G T
 TATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTCAGTGGCAGTGGATCAGGAACA
 730 740 750 760 770 780

Q Y S L K I N S L Q P E D F G S Y Y C Q
 CAATATTCTCTCAAGATCAACAGCCTGCAACCTGAAGATTTGGGAGTTATTACTGTCAA
 790 800 810 820 830 840

H F W S T P R T F G G G T K L E I K R
 CATTGGAGTACTCCTCGACGTTGGAGGCACCAAGCTGGAAATCAAACGGTAA
 850 860 870 880 890 900

TAAGAGCTCGAATT
 910

FIG. 14 b

PSW1HPOLIMYC

HindIII site AAGCTT

M K Y L L P T A A
 GCATGCAAATCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCTACGGCAGCC
 10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q
 GCTGGATTGTTATTACTCGCTGCCAACCGAGCGATGGCCAGGTGCACCTGCAG
 70 80 90 100 110 PstI

Polylinker

TCTAGA GTCGAC CTCGAG
 XbaI SalI XhoI

MYC PEPTIDE

V T V S S E O K L I S E E D L N * *
 GGTCACCGTCTCCTCAGAACAAAAACTCATCTCAGAAGAGGATCTGAATTAATAA
 BstEII

GGGCTAAGCTCGAATT

FIG. 15

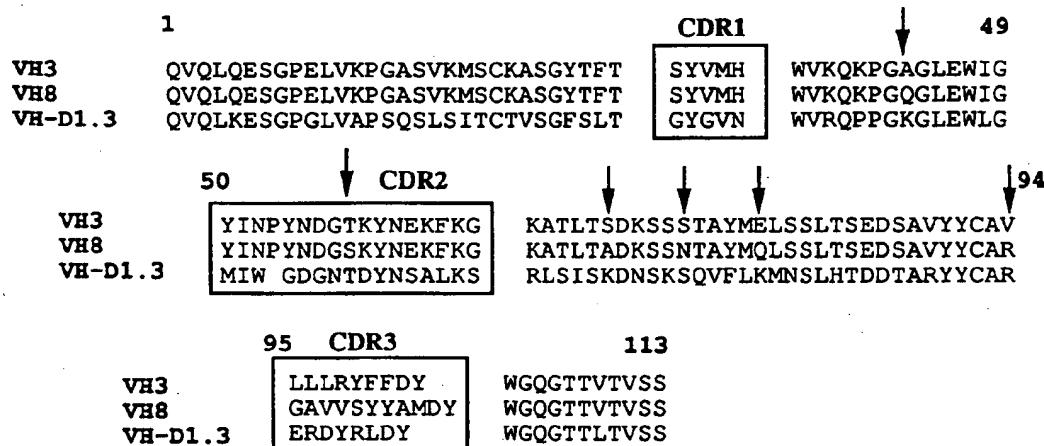


FIG. 16

FR1	QVQLQESGGGLVQPGGSLRLSCAASGFTFS	
	SYAMS	CDR1
FR2	WVRQAPGKGLEWVS	
	AISGSGGSTYYADSVKG	CDR2
FR3	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAM	
	WRGIATPVSFDLGYFDY	CDR3

FIG. 17

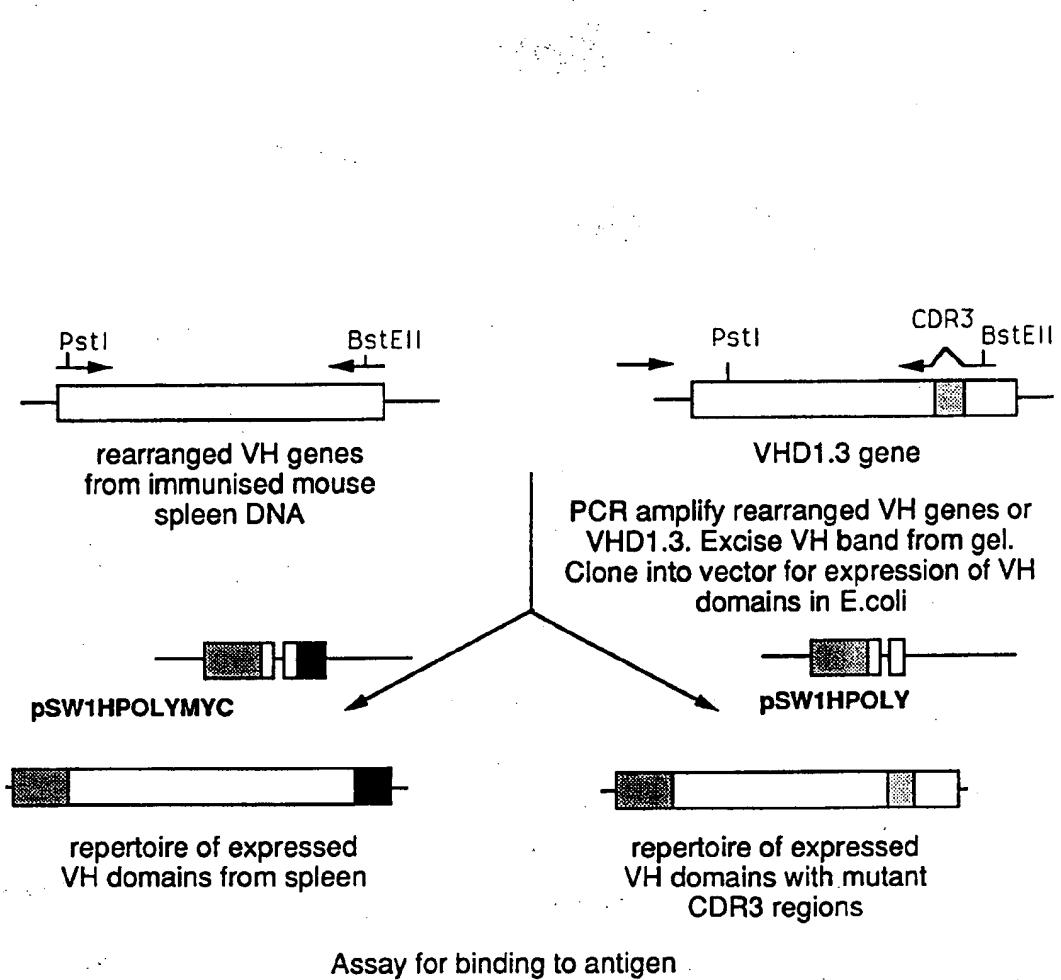


FIG. 18

pSW2HPOLY

HindIII AAGCTT

M K Y L L P T A A
 GCATGCAAATTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCAACGGCAGCC
 10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q
 GCTGGATTGTTATTACTCGCTGCCAACCGCGATGGCCAGGTGCAGCTGCAG
 70 80 90 100 110 PstI

TCTAGA GTCGAC CTCGAG
 XbaI SalI XhoI

V T V S S
 GGTCACCGTCTCCTCATAATAAGAGCTCGAATTGCCAACGCTTGATGC
 BstEII 430 440 450 460 470 480

M K Y L L P T A A A G
 AAATTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCAACGGCAGCCGCTGGA
 490 500 510 520 530 540

L L L L A A Q P A M A D I V L T Q S P A
 TTGTTATTACTCGCTGCCAACCGCGATGGCCGACATCGCCTGACTCAGTCTCCAGCC
 550 560 570 580 590 600

S L S A S V G E T V T I T C R A S G N I
 TCCCTTCTCGCTGTGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATT
 610 620 630 640 650 660

H N Y L A W Y Q Q K Q G K S P Q L L V Y
 CACAATTATTTAGCATGGTATCAGCAGAACAGGGAAAATCCTCAGCTCTGGTCTAT
 670 680 690 700 710 720

Y T T T L A D G V P S R F S G S G S G T
 TATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTTCAAGGCTGGCAGTGGATCAGGAACA
 730 740 750 760 770 780

Q Y S L K I N S L Q P E D F G S Y Y C Q
 CAATATTCTCTCAAGATCAACAGCCTGCAACCTGAAGATTGGAGTTATTACTGTCAA
 790 800 810 820 830 840

H F W S T P R T F G G G T K L E I K R
 CATTTTGGAGTACTCCTCGGACGTTGGAGGCACCAAGCTGGAAATCAAACGGTAA
 850 860 870 880 890 900

TAAGAGCTCGAATT
 910

FIG. 19

M K Y L L P T

AAGCTTGCATGCAAATTCTATTCAAGGGAGACAGTCATAATGAAATACCTATTGCCTACG
 10 20 30 40 50 60

A A A G L L L A A Q P A M A Q V Q L Q
 GCAGCCGCTGGATTGTTATTACTCGCTGCCAACCAGCGATGGCCCAGGTGCAGCTGCAG
 70 80 90 100 110 120

E S G P G L V A P S Q S L S I T C T V S
 GAGTCAGGACCTGGCCTGGTGGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCA
 130 140 150 160 170 180

G F S L T G Y G V N W V R Q P P G K G L
 GGGTTCTCATTAACCGGCTATGGTGTAAACTGGGTTGCCAGCCTCCAGGAAAGGGTCTG
 190 200 210 220 230 240

E W L G M I W G D G N T D Y N S A L K S
 GAGTGGCTGGGAATGATTGGGTGATGAAACACAGACTATAATTAGCTCTCAAATCC
 250 260 270 280 290 300

R L S I S K D N S K S Q V F L K M N S L
 AGACTGAGCATCAGCAAGGACAACCTCAAGAGCCAAGTTTTCTAAAAATGAACAGTCG
 310 320 330 340 350 360

H T D D T A R Y Y C A R E R D Y R L D Y
 CACACTGATGACACAGCAGGTACTACTGTGCCAGAGAGAGATTAGGCTTGACTAC
 370 380 390 400 410 420

W G Q G T T V T V S S G G G A P A A A P
 TGGGGCCAAGGCACCACGGTCACCGTCTCCTCAGGTGGTGGTGTCCAGCAGCTGCACCT
 430 440 450 460 470 480

A G G G Q V Q L K E S G P G L V A P S Q
 GCTGGAGGAGGACAGGTGCAGCTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAG
 490 500 510 520 530 540

S L S I T C T V S G F S L T G Y G V N W
 AGCTGTCCATCACATGCACCGTCTCAGGGTCTCATTAACCGCTATGGTGTAAACTGG
 550 560 570 580 590 600

V R Q P P G K G L E W L G M I W G D G N
 GTTCGCCAGCCTCCAGGAAGGGTCTGGAGTGGCTGGGAATGATTGGGTGATGGAAAC
 610 620 630 640 650 660

T D Y N S A L K S R L S I S K D N S K S
 ACAGACTATAATTAGCTCTCAAATCCAGACTGAGCATCAGCAAGGACAACCTCAAGAGC
 670 680 690 700 710 720

Q V F L K M N S L H T D D T A R Y Y C A
 CAAGTTTCTAAAAATGAACAGTCTGCACACTGATGACACAGGCCAGGTACTACTGTGCC
 730 740 750 760 770 780

R E R D Y R L D Y W G Q G T T V T V S S
 AGAGAGAGAGATTAGGCTTACTGGGCAAGGCACCAAGGTACCGTCTCCTCA
 790 800 810 820 830 840

* *

TAATAAGAGCTC
 850

FIG. 20

M K Y L L P T A A
 GCATGCAAATTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
 10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q E S
 GCTGGATTGTTATTACTCGCTGCCAACAGCGATGGCCAGGTGCAGCTGCAGGAGTCA
 70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
 GGACCTGGCCTGGTGGGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
 130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
 TCATTAACCGGCTATGGTGTAAACTGGGTTGCCAGCCTCAGGAAAGGGTCTGGAGTGG
 190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
 CTGGGAATGATTTGGGTGATGGAAACACAGACTATAATTCAAGCTCTCAAATCCAGACTG
 250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
 AGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTCTAAATGAACAGTCTGCACACT
 310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
 GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTACTGGGC
 370 380 390 400 410 420

Q G T T V T V S S R T P E M P V L E N R
 CAAGGCACCACGGTCACCGTCTCCTCACGGACACCAGAAATGCCCTGGAAAACCGG
 430 440 450 460 470 480

A A Q G D I T A P G G A R R L T G D Q T
 GCTGCTAGGGCGATATTACTGCACCCGGCGTGCTGCCGTTAACGGGTGATCAGACT
 490 500 510 520 530 540

A A L R D S L S D K P A K N I I L L I G
 GCCGCTCTCGTGATTCTCTTAGCGATAAACCTGCAAAAAATATTATTTGCTGATTGGC
 550 560 570 580 590 600

D G M G D S E I T A A R N Y A E G A G G
 GATGGGATGGGGACTCGGAAATTACTGCCGACGTAATTATGCCGAAGGTGCGGGCGGC
 610 620 630 640 650 660

F F K G I D A L P L T G Q Y T H Y A L N
 TTTTTAAAGGTATAGATGCCCTACCGCTTACCGGGCAATACACTCACTATGCGCTGAAT
 670 680 690 700 710 720

K K T G K P D Y V T D S A A S A T A W S
 AAAAAAACCGGCAAACCGGACTACGTCACCGACTCGGCTGCATCAGCAACCGCCTGGTCA
 730 740 750 760 770 780

FIG. 21a

T G V K T Y N G A L G V D I H E K D H P
 ACCGGTGTCAAAACCTATAACGGCGCCTGGCGTCGATATTACGAAAAAGATCACCA
 790 800 810 820 830 840

T I L E M A K A A G L A T G N V S T A E
 ACGATTCTGGAAATGGCAAAGCCGCAGGTCTGGCGACCGTAACGTTCTACCGCAGAG
 850 860 870 880 890 900

L Q D A T P A A L V A H V T S R K C Y G
 TTGCAGGATGCCACGCCGCTGCGCTGGCACATGTGACCTCGCGCAAATGCTACGGT
 910 920 930 940 950 960

P S A T S E K C P G N A L E K G G K G S
 CCGAGCGCACAGTAAAAATGTCCGGTAACGCTCTGGAAAAAGCGGAAAAGGATCG
 970 980 990 1000 1010 1020

I T E Q L L N A R A D V T L G G G A K T
 ATTACCGAACAGCTGCTAACGCTCGCAGCTACGCTTGGCGGGCGCAAAACC
 1030 1040 1050 1060 1070 1080

F A E T A T A G E W Q G K T L R E Q A Q
 TTTGCTGAAACGGCAACCGCTGGTGAATGGCAGGGAAAAACGCTGCGTGAACAGGCACAG
 1090 1100 1110 1120 1130 1140

A R G Y Q L V S D A A S L N S V T E A N
 GCGCGTGGTTATCAGTTGGTGAGCGATGCTGCCTACTGAATTGGTGAACGGAAGCGAAT
 1150 1160 1170 1180 1190 1200

Q Q K P L L G L F A D G N M P V R W L G
 CAGCAAAACCCCTGCTGGCCTGTTGCTGACGGCAATATGCCAGTGCCTGGCTAGGA
 1210 1220 1230 1240 1250 1260

P K A T Y H G N I D K P A V T C T P N P
 CCGAAAGCAACGTACCATGGCAATATCGATAAGCCCGCAGTCACCTGTACGCCAAATCCG
 1270 1280 1290 1300 1310 1320

Q R N D S V P T L A Q M T D K A I E L L
 CAACGTAATGACAGTGTACCAACCTGGCGCAGATGACCGACAAGCCATTGAATTGGT
 1330 1340 1350 1360 1370 1380

S K N E K G F F L Q V E G A S I D K Q D
 AGTAAAAATGAGAAAGGCTTTCTGCAAGTTGAAGGTGCGCTCAATCGATAAACAGGAT
 1390 1400 1410 1420 1430 1440

H A A N P C G Q I G E T V D L D E A V Q
 CATGCTGCGAACCTTGTGGCAAATTGGCGAGACGGTCGATCTCGATGAAGCCGTACAA
 1450 1460 1470 1480 1490 1500

R A L E F A K K E G N T L V I V T A D H
 CGGGCGCTGGAAATCGCTAAAAGGAGGGTAACACGCTGGTCATAGTCACCGCTGATCAC
 1510 1520 1530 1540 1550 1560

FIG. 21b

A H A S Q I V A P D T K A P G L T Q A L
GCCACGCCAGCCAGATTGTTGCCGGATACAAAGCTCCGGGCCTCACCCAGGCGCTA
1570 1580 1590 1600 1610 1620

N T K D G A V M V M S Y G N S E E D S Q
AATAACCAAAAGATGGCGCAGTGATGGTGTGAGTTACGGGAACCTCCGAAGAGGATTACAAA
1630 1640 1650 1660 1670 1680

E H T G S Q L R I A A Y G P H A A N V V
GAACATACCGGCAGTCAGTTGCGTATTGCGGCGTATGGCCCGCATGCCGCCAATGTTGTT
1690 1700 1710 1720 1730 1740

G L T D Q T D L F Y T M K A A L G L K *
GGACTGACCGGACCAAGACCGATCTCTTCTACACCATGAAAGCCGCTCTGGGGCTGAAATAA
1750 1760 1770 1780 1790 1800

AACCGCGCCCGGGAGTGAATTTCGCTGCCGGTGGTTTTGCTGTTAGC
1810 1820 1830 1840 1850

FIG. 21c

M K Y L L P T A A
 GCATGCAAATTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
 10 20 30 40 50 60

A G L L L A A Q P A M A Q V Q L Q E S
 GCTGGATTGTTATTACTCGCTGCCAACAGCGATGGCCAGGTGCAGTCAGGAGTCA
 70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
 GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
 130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
 TCATTAACCGGCTATGGTGTAAAATGGGTTGCCAGCCTCCAGGAAAGGGTCTGGAGTGG
 190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
 CTGGGAATGATTGGGGTGATGGAAACACAGACTATAATTCAAGCTCTCAAATCCAGACTG
 250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
 AGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTTCTTAAAATGAACAGTCTGCACACT
 310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
 GATGACACAGCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTIONGGGC
 370 380 390 400 410 420

Q G T T V T V S S * *
 CAAGGCACCACGGTCACCGTCTCCTCATAATAAGAGCTATCCGGGAGCTGCATGCAA
 430 440 450 460 470 480

M K Y L L P T A A A G L
 TTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTG
 490 500 510 520 530 540

L L L A A Q P A M A D I E L V D L E I K
 TTATTACTCGCTGCCAACAGCGATGGCCGACATCGAGCTCGTCGACCTCGAGATCAA
 550 560 570 580 590 600

R E Q K L I S E E D L N * *
 CGGGAACAAAACATCTCAGAAGAGGGATCTGAATTAATAATGATCAAACGGTAATAAG
 610 620 630 640 650 660

GATCCAGCTCGAATT
 670

FIG. 22

A
Q V Q L Q E S G P G L V Q P S Q S L S I
CAGGTGCAGCTGCAGGAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATC
10 20 30 40 50 60
G N P
T C T V S G F S L T S Y G V H W V R Q S
ACCTGCACAGTCTCTGGTTCTCATTAACTAGCTATGGTGTACACTGGGTTGCCAGTCT
70 80 90 100 110 120
C
P G K G L E W L G M I W G D G N T D Y N
CCAGGAAAGGGTCTGGAGTGGCTGGGAATGATTGGGGTGTGGAAACACAGACTATAAT
130 140 150 160 170 180
S A L K S R L S I S K D N S K S Q V F L
TCAGCTCTCAAATCCAGACTGAGCATCAGCAAGGACAACCCAAGAGCCAAGTTTCTTA
190 200 210 220 230 240
K M N S L H T D D T A R Y Y C A R E R D
AAAATGAACAGTCTGCACACTGATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAT
250 260 270 280 290 300
Y R L D Y W G Q G T T V T V S S
TATAGGCTTGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
310 320 330 340

FIG. 23



(19)

Europäisches Patentamt
European Patent Office
Office européen des brevets



(11) EP 0 368 684 B2

(12)

NEW EUROPEAN PATENT SPECIFICATION

(45) Date of publication and mention
of the opposition decision:
29.09.2004 Bulletin 2004/40

(51) Int Cl.7: **C07K 16/46, C12N 15/10,
C12N 15/13
// C12Q1/68**

(45) Mention of the grant of the patent:
09.03.1994 Bulletin 1994/10

(21) Application number: **89311731.7**

(22) Date of filing: **13.11.1989**

(54) Cloning immunoglobulin variable domain sequences.

Klonierung von Immunglobulin sequenzen aus den variablen Domänen.

Clonage de séquences d'immunoglobulines de domaines variables.

(84) Designated Contracting States:
AT BE CH DE ES FR GB GR IT LI LU NL SE

(30) Priority: **11.11.1988 GB 8826444
16.03.1989 GB 8906034
22.04.1989 GB 8909217
15.05.1989 GB 8911047
02.06.1989 GB 8912652
16.06.1989 GB 8913900
15.08.1989 GB 8918543**

(43) Date of publication of application:
16.05.1990 Bulletin 1990/20

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WO-A-88/01649 WO-A-88/06630

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Remarks:

The file contains technical information submitted after the application was filed and not included in this specification

Description

- [0001] The present invention relates to cloning of immunoglobulin (Ig) variable domain sequences. Methods for cloning, amplifying and expressing DNA sequences encoding at least part of an immunoglobulin variable domain and methods for the use of said DNA sequences in the production of Ig-type molecules are disclosed.
- [0002] A list of references is appended to the end of the description. The documents listed therein are referred to in the description by number, which is given in square brackets [].
- [0003] The Ig superfamily includes not only the Igs themselves but also such molecules as receptors on lymphoid cells such as T lymphocytes. Immunoglobulins comprise at least one heavy and one light chain covalently bonded together. Each chain is divided into a number of domains. At the N terminal end of each chain is a variable domain. The variable domains on the heavy and light chains fit together to form a binding site designed to receive a particular target molecule. In the case of Igs, the target molecules are antigens. T-cell receptors have two chains of equal size, the α and β chains, each consisting of two domains. At the N-terminal end of each chain is a variable domain and the variable domains on the α and β chains are believed to fit together to form a binding site for target molecules, in this case peptides presented by a histocompatibility antigen. The variable domains are so called because their amino acid sequences vary particularly from one molecule to another. This variation in sequence enables the molecules to recognise an extremely wide variety of target molecules.
- [0004] Much research has been carried out on Ig molecules to determine how the variable domains are produced. It has been shown that each variable domain comprises a number of areas of relatively conserved sequence and three areas of hypervariable sequence. The three hypervariable areas are generally known as complementarity determining regions (CDRs).
- [0005] Crystallographic studies have shown that in each variable domain of an Ig molecule the CDRs are supported on framework areas formed by the areas of conserved sequences. The three CDRs are brought together by the framework areas and, together with the CDRs on the other chain, form a pocket in which the target molecule is received.
- [0006] Since the advent of recombinant DNA technology, there has been much interest in the use of such technology to clone and express Ig molecules and derivatives thereof. This interest is reflected in the numbers of patent applications and other publications on the subject.
- [0007] The earliest work on the cloning and expression of full Igs in the patent literature is EP-A-0 120 694 (Boss). The Boss application also relates to the cloning and expression of chimeric antibodies. Chimeric antibodies are Ig-type molecules in which the variable domains from one Ig are fused to constant domains from another Ig. Usually, the variable domains are derived from an Ig from one species (often a mouse Ig) and the constant domains are derived from an Ig from a different species (often a human Ig).
- [0008] A later European patent application, EP-A-0 125 023 (Genentech), relates to much the same subject as the Boss application, but also relates to the production by recombinant DNA technology of other variations of Ig-type molecules.
- [0009] EP-A-0 194 276 (Neuberger) discloses not only chimeric antibodies of the type disclosed in the Boss application but also chimeric antibodies in which some or all of the constant domains have been replaced by non-Ig derived protein sequences. For instance, the heavy chain CH2 and CH3 domains may be replaced by protein sequences derived from an enzyme or a protein toxin.
- [0010] EP-A-0 239 400 (Winter) discloses a different approach to the production of Ig molecules. In this approach, only the CDRs from a first type of Ig are grafted onto a second type of Ig in place of its normal CDRs. The Ig molecule thus produced is predominantly of the second type, since the CDRs form a relatively small part of the whole Ig. However, since the CDRs are the parts which define the specificity of the Ig, the Ig molecule thus produced has its specificity derived from the first Ig.
- [0011] Hereinafter, chimeric antibodies, CDR-grafted Igs, the altered antibodies described by Genentech, and fragments, of such Igs such as $F(ab')_2$ and Fv fragments are referred to herein as modified antibodies.
- [0012] One of the main reasons for all the activity in the Ig field using recombinant DNA technology is the desire to use Igs in therapy. It is well known that, using the hybridoma technique developed by Kohler and Milstein, it is possible to produce monoclonal antibodies (MAbs) of almost any specificity. Thus, MAbs directed against cancer antigens have been produced. It is envisaged that these MAbs could be covalently attached or fused to toxins to provide "magic bullets" for use in cancer therapy. MAbs directed against normal tissue or cell surface antigens have also been produced. Labels can be attached to these so that they can be used for *in vivo* imaging.
- [0013] The major obstacle to the use of such MAbs in therapy or *in vivo* diagnosis is that the vast majority of MAbs which are produced are of rodent, in particular mouse, origin. It is very difficult to produce human MAbs. Since most MAbs are derived from non-human species, they are antigenic in humans. Thus, administration of these MAbs to humans generally results in an anti-Ig response being mounted by the human. Such a response can interfere with therapy or diagnosis, for instance by destroying or clearing the antibody quickly, or can cause allergic reactions or immune complex hypersensitivity which has adverse effects on the patient.

[0014] The production of modified IgS has been proposed to ensure that the Ig administered to a patient is as "human" as possible, but still retains the appropriate specificity. It is therefore expected that modified IgS will be as effective as the MAb from which the specificity is derived but at the same time not very antigenic. Thus, it should be possible to use the modified Ig a reasonable number of times in a treatment or diagnosis regime.

5 [0015] At the level of the gene, it is known that heavy chain variable domains are encoded by a "rearranged" gene which is built from three gene segments: an "unrearranged" VH gene (encoding the N-terminal three framework regions, first two complete CDRs and the first part of the third CDR), a diversity (DH)-segment (DH) (encoding the central portion of the third CDR) and a joining segment (JH) (encoding the last part of the third CDR and the fourth framework region). In the maturation of B-cells, the genes rearrange so that each unrearranged VH gene is linked to one DH gene and one JH gene. The rearranged gene corresponds to VH-DH-JH. This rearranged gene is linked to a gene which encodes the constant portion of the Ig chain.

10 [0016] For light chains, the situation is similar, except that for light chains there is no diversity region. Thus light chain variable domains are encoded by an "unrearranged" VL gene and a JL gene. There are two types of light chains, kappa (κ) or lambda (λ), which are built respectively from unrearranged $V\kappa$ genes and $J\kappa$ segments, and from unrearranged $V\lambda$ genes and $J\lambda$ segments.

15 [0017] It has been discovered that isolated Ig heavy chain variable domains can bind to antigen in a 1:1 ratio and with binding constants of equivalent magnitude to those of complete antibody molecules.

20 [0018] Single domain ligands consisting of at least part of the variable domain of one chain of a molecule from the Ig superfamily may be the end product of processes involving methods according to the present invention.

25 [0019] Preferably, each ligand consists of the variable domain of an Ig light, or, most preferably, heavy chain.

[0020] If desired, a gene for a single domain ligand can be mutated to improve the properties of the expressed domain, for example to increase the yields of expression or the solubility of the ligand, to enable the ligand to bind better, or to introduce a second site for covalent attachment (by introducing chemically reactive residues such as cysteine and histidine) or non-covalent binding of other molecules. In particular it would be desirable to introduce a second site for binding to serum components, to prolong the residence time of the domains in the serum; or for binding to molecules with effector functions, such as components of complement, or receptors on the surfaces of cells.

30 [0021] Thus, hydrophobic residues which would normally be at the interface of the heavy chain variable domain with the light chain variable domain could be mutated to more hydrophilic residues to improve solubility; residues in the CDR loops could be mutated to improve antigen binding; residues on the other loops or parts of the β -sheet could be mutated to introduce new binding activities. Mutations could include single point mutations, multiple point mutations or more extensive changes and could be introduced by any of a variety of recombinant DNA methods, for example gene synthesis, site directed mutagenesis or the polymerase chain reaction.

35 [0022] Since these ligands have equivalent binding affinity to that of complete Ig molecules, the ligands can be used in many of the ways as are Ig molecules or fragments. For example, Ig molecules have been used in therapy (such as in treating cancer, bacterial and viral diseases), in diagnosis (such as pregnancy testing), in vaccination (such as in producing anti-idiotypic antibodies which mimic antigens), in modulation of activities of hormones or growth factors, in detection, in biosensors and in catalysis.

40 [0023] It is envisaged that the small size of the ligands may confer some advantages over complete antibodies, for example, in neutralising the activity of low molecular weight drugs (such as digoxin) and allowing their filtration from the kidneys with drug attached; in penetrating tissues and tumours; in neutralising viruses by binding to small conserved regions on the surfaces of viruses such as the "canyon" sites of viruses [16]; in high resolution epitope mapping of proteins; and in vaccination by ligands which mimic antigens.

45 [0024] A single domain ligand may be linked to one or more of an effector molecule, a label, a surface, or one or more other ligands having the same or different specificity, forming a "receptor".

[0025] A receptor comprising a ligand linked to an effector molecule may be of use in therapy. The effector molecule may be a toxin, such as ricin or pseudomonas exotoxin, an enzyme which is able to activate a prodrug, a binding partner or a radio-isotope. The radio-isotope may be directly linked to the ligand or may be attached thereto by a chelating structure which is directly linked to the ligand. Such ligands with attached isotopes are much smaller than those based on Fv fragments, and could penetrate tissues and access tumours more readily.

50 [0026] A receptor comprising a ligand linked to a label may be of use in diagnosis. The label may be a heavy metal atom or a radio-isotope, in which case the receptor can be used for *in vivo* imaging using X-ray or other scanning apparatus. The metal atom or radio-isotope may be attached to the ligand either directly or via a chelating structure directly linked to the ligand. For *in vitro* diagnostic testing, the label may be a heavy metal atom, a radio-isotope, an enzyme, a fluorescent or coloured molecule or a protein or peptide tag which can be detected by an antibody, an antibody fragment or another protein. Such receptors would be used in any of the known diagnostic tests, such as ELISA or fluorescence-linked assays.

55 [0027] A receptor comprising a ligand linked to a surface, such as a chromatography medium, could be used for purification of other molecules by affinity chromatography. Linking of ligands to cells, for example to the outer membrane

proteins of *E. coli* or to hydrophobic tails which localise the ligands in the cell membranes, could allow a simple diagnostic test in which the bacteria or cells would agglutinate in the presence of molecules bearing multiple sites for binding the ligand(s).

[0028] Receptors comprising at least two ligands can be used, for instance, in diagnostic tests. The first ligand will bind to a test antigen and the second ligand will bind to a reporter molecule, such as an enzyme, a fluorescent dye, a coloured dye, a radio-isotope or a coloured-, fluorescently- or radio-labelled protein.

[0029] Alternatively, such receptors may be useful in increasing the binding to an antigen. The first ligand will bind to a first epitope of the antigen and the second ligand will bind to a second epitope. Such receptors may also be used for increasing the affinity and specificity of binding to different antigens in close proximity on the surface of cells. The first ligand will bind to the first antigen and the second epitope to the second antigen: strong binding will depend on the co-expression of the epitopes on the surface of the cell. This may be useful in therapy of tumours, which can have elevated expression of several surface markers. Further ligands could be added to further improve binding or specificity. Moreover, the use of strings of ligands, with the same or multiple specificities, creates a larger molecule which is less readily filtered from the circulation by the kidney.

[0030] For vaccination with ligands which mimic antigens, the use of strings of ligands may prove more effective than single ligands, due to repetition of the immunising epitopes.

[0031] If desired, such receptors with multiple ligands could include effector molecules or labels so that they can be used in therapy or diagnosis as described above.

[0032] The ligand may be linked to the other part of the receptor by any suitable means, for instance by covalent or non-covalent chemical linkages. However, where the receptor comprises a ligand and another protein molecule, it is preferred that they are produced by recombinant DNA technology as a fusion product. If necessary, a linker peptide sequence can be placed between the ligand and the other protein molecule to provide flexibility.

[0033] The basic techniques for manipulating Ig molecules by recombinant DNA technology are described in the patent references cited above. These may be adapted in order to allow for the production of single domain ligands and receptors by means of recombinant DNA technology.

[0034] Preferably, where the ligand is to be used for *in vivo* diagnosis or therapy in humans, it is humanised, for instance by CDR replacement as described in EP-A-0 239 400.

[0035] In order to obtain a DNA sequence encoding a ligand, it is generally necessary firstly to produce a hybridoma which secretes an appropriate MAb. This can be a very time consuming method. Once an immunised animal has been produced, it is necessary to fuse separated spleen cells with a suitable myeloma cell line, grow up the cell lines thus produced, select appropriate lines, reclone the selected lines and reselect. This can take some long time. This problem also applies to the production of modified Ig's.

[0036] A further problem with the production of ligands, and also receptors described above and modified Ig's, by recombinant DNA technology is the cloning of the variable domain encoding sequences from the hybridoma which produces the MAb from which the specificity is to be derived. This can be a relatively long method involving the production of a suitable probe, construction of a clone library from cDNA or genomic DNA, extensive probing of the clone library, and manipulation of any isolated clones to enable the cloning into a suitable expression vector. Due to the inherent variability of the DNA sequences encoding Ig variable domains, it has not previously been possible to avoid such time consuming work. It is therefore a further aim of the present invention to provide a method which enables substantially any sequence encoding an Ig superfamily molecule variable domain (ligand) to be cloned in a reasonable period of time.

[0037] According to an aspect of the present invention therefore, there is provided a method of cloning a sequence (the target sequence) which encodes at least part of the variable domain of an Ig superfamily molecule, which method comprises:

- 45 (a) providing a sample of double stranded (ds) nucleic acid which contains the target sequence;
- (b) denaturing the sample so as to separate the two strands;
- (c) annealing to the sample a forward and a back oligonucleotide primer, the forward primer being specific for a sequence at or adjacent the 3' end of the sense strand of the target sequence, the back primer being specific for a sequence at or adjacent the 3' end of the antisense strand of the target sequence, under conditions which allow the primers to hybridise to the nucleic acid at or adjacent the target sequence;
- 50 (d) treating the annealed sample with a DNA polymerase enzyme in the presence of deoxynucleoside triphosphates under conditions which cause primer extension to take place; and
- (e) denaturing the sample under conditions such that the extended primers become separated from the target sequence.

[0038] Preferably, the method of the present invention further includes the step (f) of repeating steps (c) to (e) on the denatured mixture a plurality of times.

[0039] Preferably, the method of the present invention is used to clone complete variable domains from Ig molecules, most preferably from Ig heavy chains.

[0040] In a further aspect, the invention provides an expression library comprising a repertoire of nucleic acid sequences for expression of a repertoire of proteins each comprising an immunoglobulin variable domain. The expression library may be one which comprises a repertoire of third CDR sequences, said sequences being located in an otherwise invariant VH gene.

[0041] In step (c) recited above, the forward primer becomes annealed to the sense strand of the target sequence at or adjacent the 3' end of the strand. In a similar manner, the back primer becomes annealed to the antisense strand of the target sequence at or adjacent the 3' end of the strand. Thus, the forward primer anneals at or adjacent the region of the ds nucleic acid which encodes the C terminal end of the variable region or domain. Similarly, the back primer anneals at or adjacent the region of the ds nucleic acid which encodes the N-terminal end of the variable domain.

[0042] In step (d), nucleotides are added onto the 3' end of the forward and back primers in accordance with the sequence of the strand to which they are annealed. Primer extension will continue in this manner until stopped by the beginning of the denaturing step (e). It must therefore be ensured that step (d) is carried out for a long enough time to ensure that the primers are extended so that the extended strands totally overlap one another.

[0043] In step (e), the extended primers are separated from the ds nucleic acid. The ds nucleic acid can then serve again as a substrate to which further primers can anneal. Moreover, the extended primers themselves have the necessary complementary sequences to enable the primers to anneal thereto.

[0044] During further cycles, if step (f) is used, the amount of extended primers will increase exponentially so that at the end of the cycles there will be a large quantity of cDNA having sequences complementary to the sense and antisense strands of the target sequence. Thus, the method of the present invention will result in the accumulation of a large quantity of cDNA which can form ds cDNA encoding at least part of the variable domain.

[0045] As will be apparent to the skilled person, some of the steps in the method may be carried out simultaneously or sequentially as desired.

[0046] The forward and back primers may be provided as isolated oligonucleotides, in which case only two oligonucleotides will be used. However, alternatively the forward and back primers may each be supplied as a mixture of closely related oligonucleotides. For instance, it may be found that at a particular point in the sequence to which the primer is to anneal, there is the possibility of nucleotide variation. In this case a primer may be used for each possible nucleotide variation. Furthermore it may be possible to use two or more sets of "nested" primers in the method to enhance the specific cloning of variable region genes.

[0047] The method described above is similar to the method described by Salki et al. [17]. A similar method is also used in the methods described in EP-A-0 200 362. In both cases the method described is carried out using primers which are known to anneal efficiently to the specified nucleotide sequence. In neither of these disclosures was it suggested that the method could be used to clone Ig parts of variable domain encoding sequences, where the target sequence contains inherently highly variable areas.

[0048] The ds nucleic acid sequence used in the method of the present invention may be derived from mRNA. For instance, RNA may be isolated in known manner from a cell or cell line which is known to produce Ig. mRNA may be separated from other RNA by oligo-dT chromatography. A complementary strand of cDNA may then be synthesised on the mRNA template, using reverse transcriptase and a suitable primer, to yield an RNA/DNA heteroduplex. A second strand of DNA can be made in one of several ways, for example, by priming with RNA fragments of the mRNA strand (made by incubating RNA/DNA heteroduplex with RNase H) and using DNA polymerase, or by priming with a synthetic oligodeoxynucleotide primer which anneals to the 3' end of the first strand and using DNA polymerase. It has been found that the method of the present invention can be carried out using ds cDNA prepared in this way.

[0049] When making such ds cDNA, it is possible to use a forward primer which anneals to a sequence in the CH1 domain (for a heavy chain variable domain) or the C λ or C κ domain (for a light chain variable domain). These will be located in close enough proximity to the target sequence to allow the sequence to be cloned.

[0050] The back primer may be one which anneals to a sequence at the N-terminal end of the VH1, V κ or V λ domain. The back primer may consist of a plurality of primers having a variety of sequences designed to be complementary to the various families of VH1, V κ or V λ sequences known. Alternatively the back primer may be a single primer having a consensus sequence derived from all the families of variable region genes.

[0051] Surprisingly, it has been found that the method of the present invention can be carried out using genomic DNA. If genomic DNA is used, there is a very large amount of DNA present, including actual coding sequences, introns and untranslated sequences between genes. Thus, there is considerable scope for non-specific annealing under the conditions used. However, it has surprisingly been found that there is very little non-specific annealing. It is therefore unexpected that it has proved possible to clone the genes of Ig-variable domains from genomic DNA.

[0052] Under some circumstances the use of genomic DNA may prove advantageous compared with use of mRNA, as the mRNA is readily degraded, and especially difficult to prepare from clinical samples of human tissue.

[0053] Thus, in accordance with an aspect of the present invention, the ds nucleic acid used in step (a) is genomic

DNA.

[0054] When using genomic DNA as the ds nucleic acid source, it will not be possible to use as the forward primer an oligonucleotide having a sequence complementary to a sequence in a constant domain. This is because, in genomic DNA, the constant domain genes are generally separated from the variable domain genes by a considerable number of base pairs. Thus, the site of annealing would be too remote from the sequence to be cloned.

[0055] It should be noted that the method of the present invention can be used to clone both rearranged and unrearranged variable domain sequences from genomic DNA. It is known that in germ line genomic DNA the three genes, encoding the VH, DH and JH respectively, are separated from one another by considerable numbers of base pairs. On maturation of the immune response, these genes are rearranged so that the VH, DH and JH genes are fused together to provide the gene encoding the whole variable domain (see Figure 1). By using a forward primer specific for a sequence at or adjacent the 3' end of the sense strand of the genomic "unrearranged" VH gene, it is possible to clone the "unrearranged" VH gene alone, without also cloning the DH and JH genes. This can be of use in that it will then be possible to fuse the VH gene onto pre-cloned or synthetic DH and JH genes. In this way, rearrangement of the variable domain genes can be carried out *in vitro*.

[0056] The oligonucleotide primers used in step (c) may be specifically designed for use with a particular target sequence. In this case, it will be necessary to sequence at least the 5' and 3' ends of the target sequence so that the appropriate oligonucleotides can be synthesised. However, the present inventors have discovered that it is not necessary to use such specifically designed primers. Instead, it is possible to use a species specific general primer or a mixture of such primers for annealing to each end of the target sequence. This is not particularly surprising as regards the 3' end of the target sequence. It is known that this end of the variable domain encoding sequence leads into a segment encoding JH which is known to be relatively conserved. However, it was surprisingly discovered that, within a single species, the sequence at the 5' end of the target sequence is sufficiently well conserved to enable a species specific general primer or a mixture thereof to be designed for the 5' end of the target sequence.

[0057] Therefore according to a preferred aspect of the present invention, in step (c) the two primers which are used are species specific general primers, whether used as single primers or as mixtures of primers. This greatly facilitates the cloning of any undetermined target sequence since it will avoid the need to carry out any sequencing on the target sequence in order to produce target sequence-specific primers. Thus the method of this aspect of the invention provides a general method for cloning variable region or domain encoding sequences of a particular species.

[0058] Once the variable domain gene has been cloned using the method described above, it may be directly inserted into an expression vector, for instance using the PCR reaction to paste the gene into a vector.

[0059] Advantageously, however, each primer includes a sequence including a restriction enzyme recognition site. The sequence recognised by the restriction enzyme need not be in the part of the primer which anneals to the ds nucleic acid, but may be provided as an extension which does not anneal. The use of primers with restriction sites has the advantage that the DNA can be cut with at least one restriction enzyme which leaves 3' or 5' overhanging nucleotides. Such DNA is more readily cloned into the corresponding sites on the vectors than blunt end fragments taken directly from the method. The ds cDNA produced at the end of the cycles will thus be readily insertable into a cloning vector by use of the appropriate restriction enzymes. Preferably the choice of restriction sites is such that the ds cDNA is cloned directly into an expression vector, such that the ligand encoded by the gene is expressed. In this case the restriction site is preferably located in the sequence which is annealed to the ds nucleic acid.

[0060] Since the primers may not have a sequence exactly complementary to the target sequence to which it is to be annealed, for instance because of nucleotide variations or because of the introduction of a restriction enzyme recognition site, it may be necessary to adjust the conditions in the annealing mixture to enable the primers to anneal to the ds nucleic acid. This is well within the competence of the person skilled in the art and needs no further explanation.

[0061] In step (d), any DNA polymerase may be used. Such polymerases are known in the art and are available commercially. The conditions to be used with each polymerase are well known and require no further explanation here. The polymerase reaction will need to be carried out in the presence of the four nucleoside triphosphates. These and the polymerase enzyme may already be present in the sample or may be provided afresh for each cycle.

[0062] The denaturing step (e) may be carried out, for instance, by heating the sample, by use of chaotropic agents, such as urea or guanidine, or by the use of changes in ionic strength or pH. Preferably, denaturing is carried out by heating since this is readily reversible. Where heating is used to carry out the denaturing, it will be usual to use a thermostable DNA polymerase, such as Taq polymerase, since this will not need replenishing at each cycle.

[0063] If heating is used to control the method, a suitable cycle of heating comprises denaturation at about 95°C for about 1 minute, annealing at from 30°C to 65°C for about 1 minute and primer extension at about 75°C for about 2 minutes. To ensure that elongation and renaturation is complete, the mixture after the final cycle is preferably held at about 60°C for about 5 minutes.

[0064] The product ds cDNA may be separated from the mixture for instance by gel electrophoresis using agarose gels. However, if desired, the ds cDNA may be used in unpurified form and inserted directly into a suitable cloning or expression vector by conventional methods. This will be particularly easy to accomplish if the primers include restriction

enzyme recognition sequences.

[0065] The method of the present invention may be used to make variations in the sequences encoding the variable domains. For example this may be achieved by using a mixture of related oligonucleotide primers as at least one of the primers. Preferably the primers are particularly variable in the middle of the primer and relatively conserved at the 5' and 3' ends. Preferably the ends of the primers are complementary to the framework regions of the variable domain, and the variable region in the middle of the primer covers all or part of a CDR. Preferably a forward primer is used in the area which forms the third CDR. If the method is carried out using such a mixture of oligonucleotides, the product will be a mixture of variable domain encoding sequences. Moreover, variations in the sequence may be introduced by incorporating some mutagenic nucleotide triphosphates in step (d), such that point mutations are scattered throughout 10 the target region. Alternatively such point mutations are introduced by performing a large number of cycles of amplification, as errors due to the natural error rate of the DNA polymerase are amplified, particularly when using high concentrations of nucleoside triphosphates.

[0066] The method of this aspect of the present invention has the advantage that it greatly facilitates the cloning of variable domain encoding sequences directly from mRNA or genomic DNA. This in turn will facilitate the production of 15 modified Ig-type molecules by any of the prior art methods referred to above. Further, target genes can be cloned from tissue samples containing antibody producing cells, and the genes can be sequenced. By doing this, it will be possible to look directly at the immune repertoire of a patient. This "fingerprinting" of a patient's immune repertoire could be of use in diagnosis, for instance of auto-immune diseases.

[0067] In step (a) the ds cDNA is derived from mRNA. For Ig derived variable domains, the mRNA is preferably be 20 isolated from lymphocytes which have been stimulated to enhance production of mRNA.

[0068] In each step (c) the set of primers are preferably different from the previous step (c), so as to enhance the specificity of copying. Thus the sets of primers form a nested set. For example, for cloning of Ig heavy chain variable domains, the first set of primers may be located within the signal sequence and constant region, as described by Larrick et al., [18], and the second set of primers entirely within the variable region, as described by Orlandi et al., [19]. Preferably the primers of step (c) include restriction sites to facilitate subsequent cloning. In the last cycle the set of primers used in step (c) should preferably include restriction sites for introduction into expression vectors. Possible mismatches between the primers and the template strands may be corrected by "nick translation". ds cDNA is preferably cleaved with restriction enzymes at sites introduced into the primers to facilitate the cloning.

[0069] According to another aspect of the present invention the product ds cDNA is cloned directly into an expression 30 vector. The host may be prokaryotic or eukaryotic, but is preferably bacterial. Preferably the choice of restriction sites in the primers and in the vector, and other features of the vector will allow the expression of complete ligands, while preserving all those features of the amino acid sequence which are typical of the (methoded) ligands. For example, for expression of the rearranged variable genes, the primers would be chosen to allow the cloning of target sequences including at least all the three CDR sequences. The cloning vector would then encode a signal sequence (for secretion 35 of the ligand), and sequences encoding the N-terminal end of the first framework region, restriction sites for cloning and then the C-terminal end of the last (fourth) framework region.

[0070] For expression of unrearranged VH genes as part of complete ligands, the primers would be chosen to allow the cloning of target sequences including at least the first two CDRs. The cloning vector could then encode signal sequence, the N-terminal end of the first framework region, restriction sites for cloning and then the C-terminal end of the third framework region, the third CDR and fourth framework region.

[0071] Primers and cloning vectors may likewise be devised for expression of single CDRs, particularly the third CDR, as parts of complete ligands. The advantage of cloning repertoires of single CDRs would permit the design of a "universal" set of framework regions, incorporating desirable properties such as solubility.

[0072] Single ligands could be expressed alone or in combination with a complementary variable domain. For example, a heavy chain variable domain can be expressed either as an individual domain or, if it is expressed with a complementary light chain variable domain, as an antigen binding site. Preferably the two partners would be expressed in the same cell, or secreted from the same cell, and the proteins allowed to associate non-covalently to form an Fv fragment. Thus the two genes encoding the complementary partners can be placed in tandem and expressed from a single vector, the vector including two sets of restriction sites.

[0073] Preferably the genes are introduced sequentially: for example the heavy chain variable domain can be cloned first and then the light chain variable domain. Alternatively the two genes are introduced into the vector in a single step, for example by using the polymerase chain reaction to paste together each gene with any necessary intervening sequence, as essentially described by Yon and Fried [29]. The two partners could be also expressed as a linked protein to produce a single chain Fv fragment, using similar vectors to those described above. As a further alternative the two genes may be placed in two different vectors, for example in which one vector is a phage vector and the other is a plasmid vector.

[0074] Moreover, the cloned ds cDNA may be inserted into an expression vector already containing sequences encoding one or more constant domains to allow the vector to express Ig-type chains. The expression of Fab fragments,

for example, would have the advantage over Fv fragments that the heavy and light chains would tend to associate through the constant domains in addition to the variable domains. The final expression product may be any of the modified Ig-type molecules referred to above.

[0075] The cloned sequence may also be inserted into an expression vector so that it can be expressed as a fusion protein. The variable domain encoding sequence may be linked directly or via a linker sequence to a DNA sequence encoding any protein effector molecule, such as a toxin, enzyme, label or another ligand. The variable domain sequences may also be linked to proteins on the outer side of bacteria or phage. Thus, the method of this aspect of the invention may be used to produce receptors according to the invention.

[0076] According to another aspect of the invention, the cloning of ds cDNA directly for expression permits the rapid construction of expression libraries which can be screened for binding activities. For Ig heavy and light chain variable genes, the ds cDNA may comprise variable genes isolated as complete rearranged genes from the animal, or variable genes built from several different sources, for example a repertoire of unarranged VH genes combined with a synthetic repertoire of DH and JH genes. Preferably repertoires of genes encoding Ig heavy chain variable domains are prepared from lymphocytes of animals immunised with an antigen.

[0077] The screening method may take a range of formats well known in the art. For example Ig heavy chain variable domains secreted from bacteria may be screened by binding to antigen on a solid phase, and detecting the captured domains by antibodies. Thus the domains may be screened by growing the bacteria in liquid culture and binding to antigen coated on the surface of ELISA plates. However, preferably bacterial colonies (or phage plaques) which secrete ligands (or modified ligands, or ligand fusions with proteins) are screened for antigen binding on membranes. Either the ligands are bound directly to the membranes (and for example detected with labelled antigen), or captured on antigen coated membranes (and detected with reagents specific for ligands). The use of membranes offers great convenience in screening many clones, and such techniques are well known in the art.

[0078] The screening method may also be greatly facilitated by making protein fusions with the ligands, for example by introducing a peptide tag which is recognised by an antibody at the N-terminal or C-terminal end of the ligand, or joining the ligand to an enzyme which catalyses the conversion of a colourless substrate to a coloured product. In the latter case, the binding of antigen may be detected simply by adding substrate. Alternatively, for ligands expressed and folded correctly inside eukaryotic cells, joining of the ligand and a domain of a transcriptional activator such as the GAL4 protein of yeast, and joining of antigen to the other domain of the GAL4 protein, could form the basis for screening binding activities, as described by Fields and Song [21].

[0079] The preparation of proteins, or even cells with multiple copies of the ligands, may improve the avidity of the ligand for immobilised antigen, and hence the sensitivity of the screening method. For example, the ligand may be joined to a protein subunit of a multimeric protein, to a phage coat protein or to an outer membrane protein of *E. coli* such as ompA or lamB. Such fusions to phage or bacterial proteins also offers possibilities of selecting bacteria displaying ligands with antigen binding activities. For example such bacteria may be precipitated with antigen bound to a solid support, or may be subjected to affinity chromatography, or may be bound to larger cells or particles which have been coated with antigen and sorted using a fluorescence activated cell sorter (FACS). The proteins or peptides fused to the ligands are preferably encoded by the vector, such that cloning of the ds cDNA repertoire creates the fusion product.

[0080] In addition to screening for binding activities of single ligands, it may be necessary to screen for binding or catalytic activities of associated ligands, for example, the associated Ig heavy and light chain variable domains. For example, repertoires of heavy and light chain variable genes may be cloned such that two domains are expressed together. Only some of the pairs of domains may associate, and only some of these associated pairs may bind to antigen. The repertoires of heavy and light chain variable domains could be cloned such that each domain is paired at random. This approach may be most suitable for isolation of associated domains in which the presence of both partners is required to form a cleft. Alternatively, to allow the binding of hapten. Alternatively, since the repertoires of light chain sequences are less diverse than those of heavy chains, a small repertoire of light chain variable domains, for example including representative members of each family of domains, may be combined with a large repertoire of heavy chain variable domains.

[0081] Preferably however, a repertoire of heavy chain variable domains is screened first for antigen binding in the absence of the light chain partner, and then only those heavy chain variable domains binding to antigen are combined with the repertoire of light chain variable domains. Binding of associated heavy and light chain variable domains may be distinguished readily from binding of single domains, for example by fusing each domain to a different C-terminal peptide tag which are specifically recognised by different monoclonal antibodies.

[0082] The hierarchical approach of first cloning heavy chain variable domains with binding activities, then cloning matching light chain variable domains may be particularly appropriate for the construction of catalytic antibodies, as the heavy chain may be screened first for substrate binding. A light chain variable domain would then be identified which is capable of association with the heavy chain, and "catalytic" residues such as cysteine or histidine (or prosthetic groups) would be introduced into the CDRs to stabilise the transition state or attack the substrate, as described by

Baldwin and Schultz [22].

[0083] Although the binding activities of non-covalently associated heavy and light chain variable domains (Fv fragments) may be screened, suitable fusion proteins may drive the association of the variable domain partners. Thus Fab fragments are more likely to be associated than the Fv fragments, as the heavy chain variable domain is attached to a single heavy chain constant domain, and the light chain variable domain is attached to a single light chain variable domain, and the two constant domains associate together.

[0084] Alternatively the heavy and light chain variable domains are covalently linked together with a peptide, as in the single chain antibodies, or peptide sequences attached, preferably at the C-terminal end which will associate through forming cysteine bonds or through non-covalent interactions, such as the introduction of "leucine zipper" motifs.

10 However, in order to isolate pairs of tightly associated variable domains, the Fv fragments are preferably used.

[0085] The construction of Fv fragments isolated from a repertoire of variable region genes offers a way of building complete antibodies, and an alternative to hybridoma technology. For example by attaching the variable domains to light or suitable heavy chain constant domains, as appropriate, and expressing the assembled genes in mammalian cells, complete antibodies may be made and should possess natural effector functions, such as complement lysis.

15 This route is particularly attractive for the construction of human monoclonal antibodies, as hybridoma technology has proved difficult, and for example, although human peripheral blood lymphocytes can be immortalised with Epstein Barr virus, such hybridomas tend to secrete low affinity IgM antibodies.

[0086] Moreover, it is known that immunological mechanisms ensure that lymphocytes do not generally secrete antibodies directed against host proteins. However it is desirable to make human antibodies directed against human proteins, for example to human cell surface markers to treat cancers, or to histocompatibility antigens to treat autoimmune diseases. The construction of human antibodies built from the combinatorial repertoire of heavy and light chain variable domains may overcome this problem, as it will allow human antibodies to be built with specificities which would normally have been eliminated.

20 [0087] The method also offers a new way of making bispecific antibodies. Antibodies with dual specificity can be made by fusing two hybridomas of different specificities, so as to make a hybrid antibody with an Fab arm of one specificity, and the other Fab arm of a second specificity. However the yields of the bispecific antibody are low, as heavy and light chains also find the wrong partners. The construction of Fv fragments which are tightly associated should preferentially drive the association of the correct pairs of heavy with light chains. (It would not assist in the correct pairing of the two heavy chains with each other.) The improved production of bispecific antibodies would have 25 a variety of applications in diagnosis and therapy, as is well known.

30 [0088] Thus the invention provides a species specific general oligonucleotide primer or a mixture of such primers useful for cloning variable domain encoding sequences from animals of that species. The method allows a single pair or pair of mixtures of species specific general primers to be used to clone any desired antibody specificity from that species. This eliminates the need to carry out any sequencing of the target sequence to be cloned and the need to 35 design specific primers for each specificity to be recovered.

[0089] Furthermore it provides for the construction of repertoires of variable genes, for the expression of the variable genes directly on cloning, for the screening of the encoded domains for binding activities and for the assembly of the domains with other variable domains derived from the repertoire.

40 [0090] Thus the use of the method of the present invention will allow for the production of heavy chain variable domains with binding activities and variants of these domains. It allows for the production of monoclonal antibodies and bispecific antibodies, and will provide an alternative to hybridoma technology. For instance, mouse splenic ds mRNA or genomic DNA may be obtained from a hyperimmunised mouse. This could be cloned using the method of the present invention and then the cloned ds DNA inserted into a suitable expression vector. The expression vector would be used to transform a host cell, for instance a bacterial cell, to enable it to produce an Fv fragment or a Fab 45 fragment. The Fv or Fab fragment would then be built into a monoclonal antibody by attaching constant domains and expressing it in mammalian cells.

[0091] The present invention is now described, by way of example only, with reference to the accompanying drawings in which:

50 Figure 1 shows a schematic representation of the unarranged and rearranged heavy and light chain variable genes and the location of the primers;

Figure 2 shows a schematic representation of the M13-VHPCR1 vector and a cloning scheme for amplified heavy chain variable domains;

Figure 3 shows the sequence of the Ig variable region derived sequences in M13-VHPCR1;

55 Figure 4 shows a schematic representation of the M13-VKPCR1 vector and a cloning scheme for light chain variable domains;

Figure 5 shows the sequence of the Ig variable region derived sequences in M13-VKPCR1;

Figure 6 shows the nucleotide sequences of the heavy and light chain variable domain encoding sequences of

MAb MBr1;

Figure 7 shows a schematic representation of the pSV-gpt vector (also known as α -Lys 30) which contains a variable region cloned as a HindIII-BamHI fragment, which is excised on introducing the new variable region. The gene for human IgG1 has also been engineered to remove a BamHI site, such that the BamHI site in the vector is unique;

Figure 8 shows a schematic representation of the pSV-hguro vector (also known as α -Lys 17). It is derived from pSV gpt vector with the gene encoding mycophenolic acid replaced by a gene coding for hygromycin resistance. The construct contains a variable gene cloned as a HindIII-BamHI fragment which is excised on introducing the new variable region. The gene for human C κ has also been engineered to remove a BamHI site, such that the BamHI site in the vector is unique;

Figure 9 shows the assembly of the mouse: human MBr1 chimaeric antibody;

Figure 10 shows encoded amino acid sequences of 48 mouse rearranged VH genes;

Figure 11 shows encoded amino acid sequences of human rearranged VH genes;

Figure 12 shows encoded amino acid sequences of unrearranged human VH genes;

Figure 13 shows the sequence of part of the plasmid pSW1: essentially the sequence of a pectate lyase leader linked to VHLYS in pSW1 and cloned as an SphI-EcoRI fragment into pUC19 and the translation of the open reading frame encoding the pectate lyase leader-VHLYS polypeptide being shown;

Figure 14 shows the sequence of part of the plasmid pSW2: essentially the sequence of a pectate lyase leader linked to VHLYS and to VKLYS, and cloned as an SphI-EcoRI-EcoRI fragment into pUC19 and the translation of open reading frames encoding the pectate lyase leader-VHLYS and pectate lyase leader-VKLYS polypeptides being shown;

Figure 15 shows the sequence of part of the plasmid pSW1HPOLYMYC which is based on pSW1 and in which a polylinker sequence has replaced the variable domain of VHLYS, and acts as a cloning site for amplified VH genes, and a peptide tag is introduced at the C-terminal end;

Figure 16 shows the encoded amino acid sequences of two VH domains derived from mouse spleen and having lysozyme binding activity, and compared with the VH domain of the D1,3 antibody. The arrows mark the points of difference between the two VH domains;

Figure 17 shows the encoded amino acid sequence of a VH domain derived from human peripheral blood lymphocytes and having lysozyme binding activity;

Figure 18 shows a scheme for generating and cloning mutants of the VHLYS gene, which is compared with the scheme for cloning natural repertoires of VH genes;

Figure 19 shows the sequence of part of the vector pSW2HPOLY;

Figure 20 shows the sequence of part of the vector pSW3 which encodes the two linked VHLYS domains;

Figure 21 shows the sequence of the VHLYS domain and pelB leader sequence fused to the alkaline phosphatase gene;

Figure 22 shows the sequence of the vector pSW1VHLYSVKPOLYMYC for expression of a repertoire of V κ light chain variable domains in association with the VHLYS domain; and

Figure 23 shows the sequence of VH domain which is secreted at high levels from *E. coli*. The differences with VHLYS domain are marked.

PRIMERS

[0092] In the Examples described below, the following oligonucleotide primers, or mixed primers were used. Their locations are marked on Figure 1 and sequences are as follows:

VH1FOR 5' TGAGGAGACGGTGACCGTGGTCCCTTGGCCCCAG 3';

VH1FOR-2 5' TGAGGAGACGGTGACCGTGGTCCCTTGGCCCC 3';

Hu1VHFOR 5' CTTGGTGGAGGCTGAGGAGACGGTGACC 3';

Hu2VHFOR 5' CTTGGTGGAGGCTGAGGAGACGGTGACC 3';

Hu3VHFOR 5' CTTGGTGGATGCTGAGGAGACGGTGACC 3';

Hu4VHFOR 5' CTTGGTGGATGCTGATGAGACGGTGACC 3';

5 MOJH1FOR 5' TGAGGAGACGGTGACCGTGGTCCCTGCGCCCCAG 3';
 MOJH2FOR 5' TGAGGAGACGGTGACCGTGGTGCCTGGCCCCAG 3';
 MOJH3FOR 5' TGCAGAGACGGTGACCAGAGTCCTGGCCCCAG 3';
 MOJH4FOR 5' TGAGGAGACGGTGACCGAGGTTCCCTGACCCCAG 3';

10 HUJH1FOR 5' TGAGGAGACGGTGACCAGGGTGCCCTGGCCCCAG 3';
 HUJH2FOR 5' TGAGGAGACGGTGACCAGGGTGCCACGGCCCCAG 3';
 HUJH4FOR 5' TGAGGAGACGGTGACCAGGGTTCCCTGGCCCCAG 3';

15 VK1FOR 5' GTTAGATCTCCAGCTGGTCCC 3';
 VK2FOR 5' CGTTAGATCTCCAGCTGGTCCC 3';
 20 VK3FOR 5' CCGTTCACTCGAGCTTGGTCCC 3';

25 MOJK1FOR 5' CGTTAGATCTCCAGCTTGGTGCC 3';
 MOJK3FOR 5' GGTTAGATCTCCAGTCTGGTCCC 3';
 MOJK4FOR 5' CGTTAGATCTCAAACTTGTCCC 3';

30 HUJK1FOR 5' CGTTAGATCTCACCTTGGTCCC 3';
 HUJK3FOR 5' CGTTAGATCTCCACTTGGTCCC 3';
 35 HUJK4FOR 5' CGTTAGATCTCACCTTGGTCCC 3';
 HUJK5FOR 5' CGTTAGATCTCCAGTCGTGTCCC 3';

40 VH1BACK 5' AGGT(C/G)(C/A)A(G/A)CTGCAG(G/C)AGTC(T/A)GG 3';

45 Hu2VHIBACK: 5' CAGGTGCAGCTGCAGCAGTCTGG 3';
 HuVHIIBACK: 5' CAGGTGCAGCTGCAGGAGTCGGG 3';
 Hu2VHIIIBACK: 5' GAGGTGCAGCTGCAGGAGTCTGG 3';
 50 HuVHVBACK: 5' CAGGTGCAGCTGCAGCAGTCTGG 3';

5 MOVHIBACK 5' AGGTGCAGCTGCAGGAGTCAG 3';
 MOVHIIABACK 5' AGGTCCAGCTGCAGCA(G/A)TCTGG 3';
 MOVHIIBBACK 5' AGGTCCAAGTGCAGCAGCCTGG 3';
 MOVHIIBACK 5' AGGTGAAGCTGCAGGAGTCTGG 3';

10 VK1BACK 5' GACATTCAAGCTGACCCAGTCTCCA 3';
 VK2BACK 5' GACATTGAGCTCACCCAGTCTCCA 3';

15 MOVKIIABACK 5' GATGTTCAAGCTGACCCAAACTCCA 3'
 MOVKIIIBBACK 5' GATATTCAAGCTGACCCAGGATGAA 3';

20 HuHep1FOR 5' C(A/G)(C/G)TGAGCTCACTGTGTCTCTCGCACA 3';
 HuOcta1BACK 5' CGTGAATATGCAAATAA 3';
 HuOcta2BACK 5' AGTAGGAGACATGCAAAT 3'; and
 25 HuOcta3BACK 5' CACCACCCACATGCAAAT 3';

30 VHMUT1 5' GGAGACGGTGACCGTGGTCCCTTGGCCCCAGTAGTCAAG
 NNNNNNNNNNNNNCTCTGGC 3' (where N is an
 equimolar mixture of T, C, G and A)

35 M13 PRIMER 5' AACAGCTATGACCATG 3' (New England Biolabs
 *1201)

40 EXAMPLE 1

Cloning of Mouse Rearranged Variable region genes from hybridomas, assembly of genes encoding chimaeric antibodies and the expression of antibodies from myeloma cells

45 [0093] VH1FOR is designed to anneal with the 3' end of the sense strand of any mouse heavy chain variable domain encoding sequence. It contains a BstEII recognition site. VK1FOR is designed to anneal with the 3' end of the sense strand of any mouse kappa-type light chain variable domain encoding sequence and contains a BgIII recognition site. VH1BACK is designed to anneal with the 3' end of the antisense strand of any mouse heavy chain variable domain and contains a PstI recognition site. VK1BACK is designed to anneal with the 3' end of the antisense strand of any mouse kappa-type light chain variable domain encoding sequence and contains a Pvull recognition site.

50 [0094] In this Example five mouse hybridomas were used as a source of ds nucleic acid. The hybridomas produce monoclonal antibodies (MAbs) designated MBr1 [23], BW431/26 [24], BW494/32 [25], BW250/183 [24,26] and BW704/152 [27]. MAb MBr1 is particularly interesting in that it is known to be specific for a saccharide epitope on a human mammary carcinoma line MCF-7 [28].

55 Cloning via mRNA

[0095] Each of the five hybridomas referred to above was grown up in roller bottles and about 5×10^8 cells of each

hybridoma were used to isolate RNA. mRNA was separated from the isolated RNA using oligodT cellulose [29]. First strand cDNA was synthesised according to the procedure described by Maniatis et al. [30] as set out below.

[0096] In order to clone the heavy chain variable domain encoding sequence, a 50 µl reaction solution which contains 10 µg mRNA, 20 pmole VH1FOR primer, 250 µM each of dATP, dTTP, dCTP and dGTP, 10 mM dithiothreitol (DTT), 5 100 mM Tris.HCl, 10 mM MgCl₂ and 140 mM KCl, adjusted to pH 8.3 was prepared. The reaction solution was heated at 70 °C for ten minutes and allowed to cool to anneal the primer to the 3' end of the variable domain encoding sequence in the mRNA. To the reaction solution was then added 46 units of reverse transcriptase (Anglian Biotec) and the solution was then incubated at 42°C for 1 hour to cause first strand cDNA synthesis.

[0097] In order to clone the light chain variable domain encoding sequence, the same procedure as set out above 10 was used except that the VK1FOR primer was used in place of the VH1FOR primer.

Amplification from RNA/DNA hybrid

[0098] Once the ds RNA/DNA hybrids had been produced, the variable domain encoding sequences were amplified 15 as follows. For heavy chain variable domain encoding sequence amplification, a 50 µl reaction solution containing 5 µl of the ds RNA/DNA hybrid-containing solution, 25 pmole each of VH1FOR and VH1BACK primers, 250 µM of dATP, dTTP, dCTP and dGTP, 67 mM Tris.HCl, 17 mM ammonium sulphate, 10 mM MgCl₂, 200 µg/ml gelatine and 2 units Taq polymerase (Cetus) was prepared. The reaction solution was overlaid with paraffin oil and subjected to 25 rounds of temperature cycling using a Techne PHC-1 programmable heating block. Each cycle consisted of 1 minute and 95°C (to denature the nucleic acids), 1 minute at 30°C (to anneal the primers to the nucleic acids) and 2 minutes at 72°C (to cause elongation from the primers). After the 25 cycles, the reaction solution and the oil were extracted twice with ether, once with phenol and once with phenol/CHCl₃. Thereafter ds cDNA was precipitated with ethanol. The precipitated ds cDNA was then taken up in 50 µl of water and frozen.

[0099] The procedure for light chain amplification was exactly as described above, except that the VK1FOR and 25 VK1BACK primers were used in place of the VH1FOR and VH1BACK primers respectively.

[0100] 5 µl of each sample of amplified cDNA was fractionated on 2% agarose gels by electrophoresis and stained 30 with ethidium bromide. This showed that the amplified ds cDNA gave a major band of the expected size (about 330 bp). (However the band for VK DNA of MBr1 was very weak. It was therefore excised from the gel and reamplified in a second round.) Thus by this simple procedure, reasonable quantities of ds DNA encoding the light and heavy chain variable domains of the five MAbs were produced.

Heavy Chain Vector Construction

[0101] A BstEII recognition site was introduced into the vector M13-HuVHNP [31] by site directed mutagenesis [32,33] 35 to produce the vector M13-VHPCR1 (Figures 2 and 3).

[0102] Each amplified heavy chain variable domain encoding sequence was digested with the restriction enzymes PstI and BstEII. The fragments were phenol extracted, purified on 2% low melting point agarose gels and force cloned 40 into vector M13-VHPCR1 which had been digested with PstI and BstEII and purified on an 0.8% agarose gel. Clones containing the variable domain inserts were identified directly by sequencing [34] using primers based in the 3' non-coding variable gene in the M13-VHPCR1 vector.

[0103] There is an internal PstI site in the heavy chain variable domain encoding sequences of BW431/26. This 45 variable domain encoding sequence was therefore assembled in two steps. The 3' PstI-BstEII fragment was first cloned into M13-VHPCR1, followed in a second step by the 5' PstI fragment.

Light Chain Vector Construction

[0104] Vector M13mp18 [35] was cut with Pvull and the vector backbone was blunt ligated to a synthetic HindIII-BamHI polylinker. Vector M13-HuVKLYS [36] was digested with HindIII and BamHI to isolate the HuVKLYS gene. This 50 HindIII-BamHI fragment was then inserted into the HindIII-BamHI polylinker site to form a vector M13-VKPCR1 which lacks any Pvull sites in the vector backbone (Figures 4 and 5). This vector was prepared in E Coli JM110 [22] to avoid dam methylation at the BclI site.

[0105] Each amplified light chain variable domain encoding sequence was digested with Pvull and BglII. The fragments were phenol extracted, purified on 2% low melting point agarose gels and force cloned into vector M13-VKPCR1 55 which had been digested with Pvull and BclI, purified on an 0.8% agarose gel and treated with calf intestinal phosphatase. Clones containing the light chain variable region inserts were identified directly by sequencing [34] using primers based in the 3' non-coding region of the variable domain in the M13-VKPCR1 vector.

[0106] The nucleotide sequences of the MBr1 heavy and light chain variable domains are shown in Figure 6 with part of the flanking regions of the M13-VHPCR1 and M13-VKPCR1 vectors.

Antibody Expression

[0107] The HindIII-BamHI fragment carrying the MBr1 heavy chain variable domain encoding sequence in M13-VHPCR1 was recloned into a pSV-gpt vector with human $\gamma 1$ constant regions [37] (Figure 7). The MBr1 light chain variable domain encoding sequence in M13-VKPCR1 was recloned as a HindIII-BamHI fragment into a pSV vector, pSV-hyg-HUCK with a hygromycin resistance marker and a human kappa constant domain (Figure 8). The assembly of the genes is summarised in Figure 9.

[0108] The vectors thus produced were linearised with PvuI (in the case of the pSV-hygro vectors the PvuI digest is only partial) and cotransfected into the non-secreting mouse myeloma line NSO [38] by electroporation [39]. One day after cotransfection, cells were selected in 0.3 μ g/ml mycophenolic acid (MPA) and after seven days in 1 μ g/ml MPA. After 14 days, four wells, each containing one or two major colonies, were screened by incorporation of 14 C-lysine [40] and the secreted antibody detected after precipitation with protein-A SepharoseTM (Pharmacia) on SDS-PAGE [41]. The gels were stained, fixed, soaked in a fluorographic reagent, AmplifyTM (Amersham), dried and autoradiographed on preflashed film at -70°C for 2 days.

[0109] Supernatant was also tested for binding to the mammary carcinoma line MCF-7 and the colon carcinoma line HT-29, essentially as described by Menard et al. [23], either by an indirect immunofluorescence assay on cell suspensions (using a fluorescein-labelled goat anti-human IgG (Amersham)) or by a solid phase RIA on monolayers of fixed cells (using 125 I-protein A (Amersham)).

[0110] It was found that one of the supernatants from the four wells contained secreted antibody. The chimeric antibody in the supernatant, like the parent mouse MBr1 antibody, was found to bind to MCF-7 cells but not the HT-29 cells, thus showing that the specificity had been properly cloned and expressed.

Example 2Cloning of rearranged variable genes from genomic DNA of mouse spleenPreparation of DNA from spleen.

[0111] The DNA from the mouse spleen was prepared in one of two ways (although other ways can be used).

[0112] Method 1. A mouse spleen was cut into two pieces and each piece was put into a standard Eppendorf tube with 200 μ l of PBS. The tip of a 1 ml glass pipette was closed and rounded in the blue flame of a Bunsen burner. The pipette was used to squash the spleen piece in each tube. The cells thus produced were transferred to a fresh Eppendorf tube and the method was repeated three times until the connective tissue of the spleen appeared white. Any connective tissue which has been transferred with the cells was removed using a drawn-out Pasteur pipette. The cells were then washed in PBS and distributed into four tubes.

[0113] The mouse spleen cells were then sedimented by a 2 minute spin in a Microcentaur centrifuge at low speed setting. All the supernatant was aspirated with a drawn out Pasteur pipette. If desired, at this point the cell sample can be frozen and stored at -20 °C

[0114] To the cell sample (once thawed if it had been frozen) was added 500 μ l of water and 5 μ l of a 10% solution of NP-40, a non-ionic detergent. The tube was closed and a hole was punched in the lid. The tube was placed on a boiling water bath for 5 minutes to disrupt the cells and was then cooled on ice for 5 minutes. The tube was then spun for 2 minutes at high speed to remove cell debris.

[0115] The supernatant was transferred to a new tube and to this was added 125 μ l 5M NaCl and 30 μ l 1M MOPS adjusted to pH 7.0. The DNA in the supernatant was absorbed on a Quiagen 5 tip and purified following the manufacturer's instructions for lambda DNA. After isopropanol precipitation, the DNA was resuspended in 500 μ l water.

[0116] Method 2. This method is based on the technique described in Maniatis et al. [30]. A mouse spleen was cut into very fine pieces and put into a 2 ml glass homogeniser. The cells were then freed from the tissue by several slow up and down strokes with the piston. The cell suspension was made in 500 μ l phosphate buffered saline (PBS) and transferred to an Eppendorf tube. The cells were then spun for 2 min at low speed in a Microcentaur centrifuge. This results in a visible separation of white and red cells. The white cells, sedimenting slower, form a layer on top of the red cells. The supernatant was carefully removed and spun to ensure that all the white cells had sedimented. The layer of white cells was resuspended in two portions of 500 μ l PBS and transferred to another tube.

[0117] The white cells were precipitated by spinning in the Microcentaur centrifuge at low speed for one minute. The cells were washed a further two times with 500 μ l PBS, and were finally resuspended in 200 μ l PBS. The white cells were added to 2.5 ml 25 mM EDTA and 10 mM Tris.Cl, pH 7.4, and vortexed slowly. While vortexing 25 μ l 20% SDS was added. The cells lysed immediately and the solution became viscous and clear. 100 μ l of 20 mg/ml proteinase K was added and incubated one to three hours at 50 °C.

[0118] The sample was extracted with an equal volume of phenol and the same volume of chloroform, and vortexed.

After centrifuging, the aqueous phase was removed and 1/10 volume 3M ammonium acetate was added. This was overlaid with three volumes of cold ethanol and the tube rocked carefully until the DNA strands became visible. The DNA was spooled out with a Pasteur pipette, the ethanol allowed to drip off, and the DNA transferred to 1 ml of 10 mM Tris.Cl pH 7.4, 0.1 mM EDTA in an Eppendorf tube. The DNA was allowed to dissolve in the cold overnight on a roller.

5

Amplification from genomic DNA.

[0119] The DNA solution was diluted 1/10 in water and boiled for 5 min prior to using the polymerase chain reaction (PCR). For each PCR reaction, typically 50-200 ng of DNA were used.

10

[0120] The heavy and light chain variable domain encoding sequences in the genomic DNA isolated from the human PBL or the mouse spleen cells was then amplified and cloned using the general protocol described in the first two paragraphs of the section headed "Amplification from RNA/DNA Hybrid" in Example 1, except that during the annealing part of each cycle, the temperature was held at 65°C and that 30 cycles were used. Furthermore, to minimise the annealing between the 3' ends of the two primers, the sample was first heated to 95°C, then annealed at 65°C, and only then was the Taq polymerase added. At the end of the 30 cycles, the reaction mixture was held at 60°C for five minutes to ensure that complete elongation and renaturation of the amplified fragments had taken place.

15

[0121] The primers used to amplify the mouse spleen genomic DNA were VH1FOR and VH1BACK, for the heavy chain variable domain and VK2FOR and VK1BACK, for the light chain variable domain. (VK2FOR only differs from VK1FOR in that it has an extra C residue on the 5' end.)

20

[0122] Other sets of primers, designed to optimise annealing with different families of mouse VH and Vx genes were devised and used in mixtures with the primers above. For example, mixtures of VK1FOR, MOJK1FOR, MOJK3FOR and MOJK4FOR were used as forward primers and mixtures of VK1BACK, MOVKIIABACK and MOVKIIIBACK as back primers for amplification of Vx genes. Likewise mixtures of VH1FOR, MOJH1FOR, MOJH2FOR, MOJH3FOR and MOJH4FOR were used as forward primers and mixtures of VH1BACK, MOVHIBACK, MOVHIIABACK, MOVHIIIBACK, MOVHIIIBACK were used as backward primers for amplification of VH genes.

25

[0123] All these heavy chain FOR primers referred to above contain a BstEII site and all the BACK primers referred to above contain a PstI site. These light chain FOR and BACK primers referred to above all contain BgIII and Pvull sites respectively. Light chain primers (VK3FOR and VK2BACK) were also devised which utilised different restriction sites, SacI and Xhol.

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[0124] Typically all these primers yielded amplified DNA of the correct size on gel electrophoresis, although other bands were also present. However, a problem was identified in which the 5' and 3' ends of the forward and backward primers for the VH genes were partially complementary, and this could yield a major band of "primer-dimer" in which the two oligonucleotides prime on each other. For this reason an improved forward primer, VH1FOR-2 was devised in which the two 3' nucleotides were removed from VH1FOR.

35

[0125] Thus, the preferred amplification conditions for mouse VH genes are as follows: the sample was made in a volume of 50-100 µl, 50-100 ng of DNA, VH1 FOR-2 and VH1 BACK primers (25 pmole of each), 250 µM of each deoxynucleotide triphosphate, 10 mM Tris.HCl, pH 8.8, 50 mM KCl, 1.5 mM MgCl₂, and 100 µg/ml gelatine. The sample was overlaid with paraffin oil, heated to 95° C for 2 min, 65° C for 2 min, and then to 72°C: taq polymerase was added after the sample had reached the elongation temperature and the reaction continued for 2 min at 72° C. The sample was subjected to a further 29 rounds of temperature cycling using the Techne PHC-1 programmable heating block.

40

[0126] The preferred amplification conditions for mouse Vk genes from genomic DNA are as follows: the sample treated as above except with Vk primers, for example VK3FOR and VK2BACK, and using a cycle of 94° C for one minute, 60° C for one minute and 72° C for one minute.

45

[0127] The conditions which were devised for genomic DNA are also suitable for amplification from the cDNA derived from mRNA from mouse spleen or mouse hybridoma.

Cloning and analysis of variable region genes

50

[0128] The reaction mixture was then extracted twice with 40 µl of water-saturated diethyl ether. This was followed by a standard phenol extraction and ethanol precipitation as described in Example 1. The DNA pellet was then dissolved in 100 µl 10 mM Tris.Cl, 0.1 mM EDTA.

55

[0129] Each reaction mixture containing a light chain variable domain encoding sequence was digested with SacI and Xhol (or with Pvull and BgIII) to enable it to be ligated into a suitable expression vector. Each reaction mixture containing a heavy chain variable domain encoding sequence was digested with PstI and BstEII for the same purpose.

[0130] The heavy chain variable genes isolated as above from a mouse hyperimmunised with lysozyme were cloned into M13VHPCR1 vector and sequenced. The complete sequences of 48 VH gene clones were determined (Figure 10). All but two of the mouse VH gene families were represented, with frequencies of: VA (1), IIIC (1), IIIB (8), IIIA (3), IIB (17), IIA (2), IB (12), IA (4). In 30 clones, the D segments could be assigned to families SP2 (14), FL16 (11) and

Q52 (5), and in 38 clones the JH minigenes to families JH1 (3), JH2 (7), JH3 (14) and JH4 (14). The different sequences of CDR3 marked out each of the 48 clones as unique. Nine pseudogenes and 16 unproductive rearrangements were identified. Of the clones sequenced, 27 have open reading frames.

5 [0131] Thus the method is capable of generating a diverse repertoire of heavy chain variable genes from mouse spleen DNA.

Example 3

Cloning of rearranged variable genes from mRNA from human peripheral blood lymphocytes

Preparation of mRNA.

[0132] Human peripheral blood lymphocytes were purified and mRNA prepared directly (Method 1), or mRNA was prepared after addition of Epstein Barr virus (Method 2).

15 [0133] Method 1. 20 ml of heparinised human blood from a healthy volunteer was diluted with an equal volume of phosphate buffered saline (PBS) and distributed equally into 50 ml Falcon tubes. The blood was then underlaid with 15ml Ficoll-Hypaque (Pharmacia 10-A-001-07). To separate the lymphocytes from the red blood cells, the tubes were spun for 10 minutes at 1800 rpm at room temperature in an IEC Centra 3E table centrifuge. The peripheral blood lymphocytes (PBL) were then collected from the interphase by aspiration with a Pasteur pipette. The cells were diluted with an equal volume of PBS and spun again at 1500 rpm for 15 minutes. The supernatant was aspirated, the cell pellet was resuspended in 1 ml PBS and the cells were distributed into two Eppendorf tubes.

20 [0134] Method 2. 40 ml human blood from a patient with HIV in the pre-AIDS condition was layered on Ficoll to separate the white cells (see Method 1 above). The white cells were then incubated in tissue culture medium for 4-5 days. On day 3, they were infected with Epstein Barr virus. The cells were pelleted (approx 2×10^7 cells) and washed in PBS.

25 [0135] The cells were pelleted again and lysed with 7 ml 5M guanidine isothiocyanate, 50 mM Tris, 10 mM EDTA, 0.1 mM dithiothreitol. The cells were vortexed vigorously and 7 volumes of 4M LiCl added. The mixture was incubated at 4°C for 15-20 hrs. The suspension was spun and the supernatant resuspended in 3M LiCl and centrifuged again. The pellet was dissolved in 2ml 0.1 % SDS, 10 mM Tris HCl and 1 mM EDTA. The suspension was frozen at -20°C, and thawed by vortexing for 20 s every 10 min for 45 min. A large white pellet was left behind and the clear supernatant was extracted with phenol chloroform, then with chloroform. The RNA was precipitated by adding 1/10 volume 3M sodium acetate and 2 vol ethanol and leaving overnight at -20°C. The pellet was suspended in 0.2 ml water and reprecipitated with ethanol. Aliquots for cDNA synthesis were taken from the ethanol precipitate which had been vortexed to create a fine suspension.

30 [0136] 100 µl of the suspension was precipitated and dissolved in 20 µl water for cDNA synthesis [30] using 10 pmole of a HUFOR primer (see below) in final volume of 50 µl. A sample of 5 µl of the cDNA was amplified as in Example 2 except using the primers for the human VH gene families (see below) using a cycle of 95°C, 60°C and 72°C.

35 [0137] The back primers for the amplification of human DNA were designed to match the available human heavy and light chain sequences, in which the different families have slightly different nucleotide sequences at the 5' end. Thus for the human VH genes, the primers Hu2VHIBACK, HuVHIBACK, Hu2VHIIIBACK and HuVH1VBACK were designed as back primers, and HUJH1FOR, HUJH2FOR and HUJH4FOR as forward primers based entirely in the variable gene. Another set of forward primers Hu1VHFOR, Hu2VHFOR, Hu3VHFOR, and Hu4VHFOR was also used, which were designed to match the human J-regions and the 5' end of the constant regions of different human isotopes.

40 [0138] Using sets of these primers it was possible to demonstrate a band of amplified ds cDNA by gel electrophoresis.

45 [0139] One such experiment was analysed in detail to establish whether there was a diverse repertoire in a patient with HIV infection. It is known that during the course of AIDS, that T-cells and also antibodies are greatly diminished in the blood. Presumably the repertoire of lymphocytes is also diminished. In this experiment, for the forward priming, an equimolar mixture of primers Hu1VHFOR, Hu2VHFOR, Hu3VHFOR, and Hu4VHFOR (in PCR 25 pmole of primer 5' ends) was used. For the back priming, the primers Hu2VHIBACK, HuVHIBACK, Hu2VHIIIBACK and HuVH1VBACK were used separately in four separate primings. The amplified DNA from the separate primings was then pooled, digested with restriction enzymes PstI and BstEII as above, and then cloned into the vector M13VHPCR1 for sequencing. The sequences reveal a diverse repertoire (Fig. 11) at this stage of the disease.

50 [0140] For human Vx genes the primers HuJK1FOR, HUJK3FOR, HUJK4FOR and HUJK5FOR were used as forward primers and VK1BACK as back primer. Using these primers it was possible to see a band of amplified ds cDNA of the correct size by gel electrophoresis.

Example 4Cloning of unarranged variable gene genomic DNA from human peripheral blood lymphocytes

- 5 [0141] Human peripheral blood lymphocytes of a patient with non-Hodgkins lymphoma were prepared as in Example 3 (Method 1). The genomic DNA was prepared from the PBL using the technique described in Example 2 (Method 2). The VH region in the isolated genomic DNA was then amplified and cloned using the general protocol described in the first two paragraphs of the section headed "Amplification from RNA/DNA hybrid" in Example 1 above, except that during the annealing part of each cycle, the temperature was held at 55°C and that 30 cycles were used. At the end of the
10 30 cycles, the reaction mixture was held at 60°C for five minutes to ensure that complete elongation and renaturation of the amplified fragments had taken place.
- [0142] The forward primer used was HuHep1FOR, which contains a SacI site. This primer is designed to anneal to the 3' end of the unarranged human VH region gene, and in particular includes a sequence complementary to the last three codons in the VH region gene and nine nucleotides downstream of these three codons.
- 15 [0143] As the back primer, an equimolar mixture of HuOcta1BACK, HuOcta2BACK and HuOcta3BACK was used. These primers anneal to a sequence in the promoter region of the genomic DNA VH gene (see Figure 1). 5µl of the amplified DNA was checked on 2% agarose gels in TBE buffer and stained with ethidium bromide. A double band was seen of about 620 nucleotides which corresponds to the size expected for the unarranged VH gene. The ds cDNA was digested with SacI and cloned into an M13 vector for sequencing. Although there are some sequences which are
20 identical, a range of different unarranged human VH genes were identified (Figure 12).

Example 5Cloning Variable Domains with Binding Activities from a Hybridoma

- 25 [0144] The heavy chain variable domain (VHLYS) of the D1.3 (anti-lysozyme) antibody was cloned into a vector similar to that described previously [42] but under the control of the lac z promoter, such that the VHLYS domain is attached to a pelB leader sequence for export into the periplasm. The vector was constructed by synthesis of the pelB leader sequence [43], using overlapping oligonucleotides, and cloning into a pUC 19 vector [35]. The VHLYS domain of the D1.3 antibody was derived from a cDNA clone [44] and the construct (pSW1) sequenced (Figure 13).
- 30 [0145] To express both heavy and light chain variable domains together, the light chain variable region (VKLYS) of the D1.3 antibody was introduced into the pSW1 vector, with a pelB signal sequence to give the construct pSW2 (Figure 14).
- 35 [0146] A strain of E. coli (BMH71-18) [45] was then transformed [46,47] with the plasmid pSW1 or pSW2, and colonies resistant to ampicillin (100 µg/ml) were selected on a rich (2 x TY = per litre of water, 16g Bactotryptone, 10g yeast extract, 5g NaCl) plate which contained 1% glucose to repress the expression of variable domain(s) by catabolite repression.
- 40 [0147] The colonies were inoculated into 50 ml 2 x TY (with 1% glucose and 100 µg/ml ampicillin) and grown in flasks at 37°C with shaking for 12-16 hr. The cells were centrifuged, the pellet washed twice with 50 mM sodium chloride, resuspended in 2 x TY medium containing 100 µg/ml ampicillin and the inducer IPTG (1 mM) and grown for a further 30 hrs at 37°C. The cells were centrifuged and the supernatant was passed through a Nalgene filter (0.45 µm) and then down a 1 - 5 ml lysozyme-Sepharose affinity column. (The column was derived by coupling lysozyme at 10 mg/ml to CNBr activated Sepharose.) The column was first washed with phosphate buffered saline (PBS), then with 50 mM diethylamine to elute the VHLYS domain (from pSW1) or VKLYS in association with VKLYS (from pSW2).
- 45 [0148] The VHLYS and VKLYS domains were identified by SDS polyacrylamide electrophoresis as the correct size. In addition, N-terminal sequence determination of VHLYS and VKLYS isolated from a polyacrylamide gel showed that the signal peptide had been produced correctly. Thus both the Fv fragment and the VHLYS domains are able to bind to the lysozyme affinity column, suggesting that both retain at least some of the affinity of the original antibody.
- 50 [0149] The size of the VHLYS domain was compared by FPLC with that of the Fv fragment on Superose 12. This indicates that the VHLYS domain is a monomer. The binding of the VHLYS and Fv fragment to lysozyme was checked by ELISA, and equilibrium and rapid reaction studies were carried out using fluorescence quench.
- [0150] The ELISA for lysozyme binding was undertaken as follows:
- (1) The plates (Dynatech Immulon) were coated with 200 µl per well of 300 µg/ml lysozyme in 50 mM NaHCO₃, pH 9.6 overnight at room temperature;
- 55 (2) The wells were rinsed with three washes of PBS, and blocked with 300 µl per well of 1% Sainsbury's instant dried skimmed milk powder in PBS for 2 hours at 37°C;
- (3) The wells were rinsed with three washes of PBS and 200 µl of VHLYS or Fv fragment (VHLYS associated with

VKLYS) were added and incubated for 2 hours at room temperature;

(4) The wells were washed three times with 0.05% Tween 20 in PBS and then three times with PBS to remove detergent;

5 (5) 200 µl of a suitable dilution (1:1000) of rabbit polyclonal antisera raised against the FV fragment in 2% skimmed milk powder in PBS was added to each well and incubated at room temperature for 2 hours;

(6) Washes were repeated as in (4);

10 (7) 200 µl of a suitable dilution (1:1000) of goat anti-rabbit antibody (ICN Immunochemicals) coupled to horse radish peroxidase, in 2% skimmed milk powder in PBS, was added to each well and incubated at room temperature for 1 hour;

(8) Washes were repeated as in (4); and

15 (9) 200 µl 2,2'azino-bis(3-ethylbenzthiazolinesulphonic acid) [Sigma] (0.55 mg/ml, with 1 µl 20% hydrogen peroxide: water per 10 ml) was added to each well and the colour allowed to develop for up to 10 minutes at room temperature.

[0151] The reaction was stopped by adding 0.05% sodium azide in 50 mM citric acid pH 4.3. ELISA plates were read in a Titertek Multiscan plate reader. Supernatant from the induced bacterial cultures of both pSW1 (VHLYS domain) or pSW2 (Fv fragment) was found to bind to lysozyme in the ELISA.

[0152] The purified VHLYS and Fv fragments were titrated with lysozyme using fluorescence quench (Perkin Elmer LS5B Luminescence Spectrometer) to measure the stoichiometry of binding and the affinity constant for lysozyme 20 [48,49]. The titration of the Fv fragment at a concentration of 30 nM indicates a dissociation constant of 2.8 nM using a Scatchard analysis.

[0153] A similar analysis using fluorescence quench and a Scatchard plot was carried out for VHLYS, at a VHLYS concentration of 100 nM. The stoichiometry of antigen binding is about 1 mole of lysozyme per mole of VHLYS (calculated from plot). (The concentration of VH domains was calculated from optical density at 280 nM using the typical extinction coefficient for complete immunoglobulins.) Due to possible errors in measuring low optical densities and the assumption about the extinction coefficient, the stoichiometry was also measured more carefully. VHLYS was titrated with lysozyme as above using fluorescence quench. To determine the concentration of VHLYS a sample of the stock solution was removed, a known amount of norleucine added, and the sample subjected to quantitative amino acid analysis. This showed a stoichiometry of 1.2 mole of lysozyme per mole of VHLYS domain. The dissociation constant 25 was calculated at about 12 nM.

[0154] The on-rates for VHLYS and Fv fragments with lysozyme were determined by stopped-flow analysis (HI Tech Stop Flow SHU machine) under pseudo-first order conditions with the fragment at a ten fold higher concentration than lysozyme [50]. The concentration of lysozyme binding sites was first measured by titration with lysozyme using fluorescence quench as above. The on rates were calculated per mole of binding site (rather than amount of VHLYS protein). The on-rate for the Fv fragment was found to be $2.2 \times 10^6 \text{ M}^{-1}\text{s}^{-1}$ at 25°C. The on-rate for the VHLYS fragment found to be $3.8 \times 10^6 \text{ M}^{-1} \text{ s}^{-1}$ and the off-rate 0.075 s⁻¹ at 20°C. The calculated affinity constant is 19 nM. Thus the VHLYS binds to lysozyme with a dissociation constant of about 19 nM, compared with that of the Fv of 3 nM.

Example 6

40 Cloning complete variable domains with binding activities from mRNA or DNA of antibody-secreting cells

[0155] A mouse was immunised with hen egg white lysozyme (100 µg i.p. day 1 in complete Freunds adjuvant), after 45 14 days immunised i.p. again with 100 µg lysozyme with incomplete Freunds adjuvant, and on day 35 i.v. with 50 µg lysozyme in saline. On day 39, spleen was harvested. A second mouse was immunised with keyhole limpet haemocyanin (KLH) in a similar way. The DNA was prepared from the spleen according to Example 2 (Method 2). The VH genes were amplified according to the preferred method in Example 2.

[0156] Human peripheral blood lymphocytes from a patient infected with HIV were prepared as in Example 3 (Method 50 2) and mRNA prepared. The VH genes were amplified according to the method described in Example 3, using primers designed for human VH gene families.

[0157] After the PCR, the reaction mixture and oil were extracted twice with ether, once with phenol and once with phenol/CHCl₃. The double stranded DNA was then taken up in 50 µl of water and frozen. 5 µl was digested with PstI and BstEII (encoded within the amplification primers) and loaded on an agarose gel for electrophoresis. The band of amplified DNA at about 350 bp was extracted.

55 Expression of anti-lysozyme activities

[0158] The repertoire of amplified heavy chain variable domains (from mouse immunised with lysozyme and from

human PBLs) was then cloned directly into the expression vector pSW1HPOLYMYC. This vector is derived from pSW1 except that the VHLYS gene has been removed and replaced by a polylinker restriction site. A sequence encoding a peptide tag was inserted (Figure 15). Colonies were toothpicked into 1 ml cultures. After induction (see Example 5 for details), 10 µl of the supernatant from fourteen 1 ml cultures was loaded on SDS-PAGE gels and the proteins transferred electrophoretically to nitrocellulose. The blot was probed with antibody 9E10 directed against the peptide tag.

[0159] The probing was undertaken as follows. The nitrocellulose filter was incubated in 3% bovine serum albumin (BSA)/TBS buffer for 20 min (10 x TBS buffer is 100 mM Tris.HCl, pH 7.4, 9% w/v NaCl). The filter was incubated in a suitable dilution of antibody 9E10 (about 1/500) in 3% BSA/TBS for 1 - 4 hrs. After three washes in TBS (100 ml per wash, each wash for 10 min), the filter was incubated with 1:500 dilution of anti-mouse antibody (peroxidase conjugated anti-mouse Ig (Dakopats)) in 3% BSA/TBS for 1 - 2 hrs. After three washes in TBS and 0.1% Triton X-100 (about 100 ml per wash, each wash for 10 min), a solution containing 10 ml chloronaphthol in methanol (3 mg/ml), 40 ml TBS and 50 µl hydrogen peroxide solution was added over the blot and allowed to react for up to 10 min. The substrate was washed out with excess water. The blot revealed bands similar in mobility to VHLYSMYC on the Western blot, showing that other VH domains could be expressed.

[0160] Colonies were then toothpicked individually into wells of an ELISA plate (200 µl) for growth and induction. They were assayed for lysozyme binding with the 9E10 antibody (as in Examples 5 and 7). Wells with lysozyme-binding activity were identified. Two positive wells (of 200) were identified from the amplified mouse spleen DNA and one well from the human cDNA. The heavy chain variable domains were purified on a column of lysozyme-Sepharose. The affinity for lysozyme of the clones was estimated by fluorescence quench titration as >50nM. The affinities of the two clones (VH3 and VH8) derived from the mouse genes were also estimated by stop flow analysis (ratio of k_{on}/k_{off}) as 12 nM and 27 nM respectively. Thus both these clones have a comparable affinity to the VHLYS domain. The encoded amino acid sequences of VH3 and VH8 are given in Figure 16, and that of the human variable domain in Figure 17.

[0161] A library of VH domains made from the mouse immunised with lysozyme was screened for both lysozyme and keyhole limpet haemocyanin (KLH) binding activities. Two thousand colonies were toothpicked in groups of five into wells of ELISA plates, and the supernatants tested for binding to lysozyme coated plates and separately to KLH coated plates. Twenty one supernatants were shown to have lysozyme binding activities and two to have KLH binding activities. A second expression library, prepared from a mouse immunised with KLH was screened as above. Fourteen supernatants had KLH binding activities and a single supernatant had lysozyme binding activity.

[0162] This shows that antigen binding activities can be prepared from single VH domains, and that immunisation facilitates the isolation of these domains.

Example 7

Cloning variable domains with binding activities by mutagenesis.

[0163] Taking a single rearranged VH gene, it may be possible to derive entirely new antigen binding activities by extensively mutating each of the CDRs. The mutagenesis might be entirely random, or be derived from pre-existing repertoires of CDRs. Thus a repertoire of CDR3s might be prepared as in the preceding examples by using "universal" primers based in the flanking sequences, and likewise repertoires of the other CDRs (singly or in combination). The CDR repertoires could be stitched into place in the flanking framework regions by a variety of recombinant DNA techniques.

[0164] CDR3 appears to be the most promising region for mutagenesis as CDR3 is more variable in size and sequence than CDRs 1 and 2. This region would be expected to make a major contribution to antigen binding. The heavy chain variable region (VHLYS) of the anti-lysozyme antibody D1.3 is known to make several important contacts in the CDR3 region.

[0165] Multiple mutations were made in CDR3. The polymerase chain reaction (PCR) and a highly degenerate primer were used to make the mutations and by this means the original sequence of CDR3 was destroyed. (It would also have been possible to construct the mutations in CDR3 by cloning a mixed oligonucleotide duplex into restriction sites flanking the CDR or by other methods of site-directed mutagenesis). Mutants expressing heavy chain variable domains with affinities for lysozyme were screened and those with improved affinities or new specificities were identified.

[0166] The source of the heavy chain variable domain was an M13 vector containing the VHLYS gene. The body of the sequence encoding the variable region was amplified using the polymerase chain reaction (PCR) with the mutagenic primer VHMUT1 based in CDR3 and the M13 primer which is based in the M13 vector backbone. The mutagenic primer hypermutates the central four residues of CDR3 (Arg-Asp-Tyr-Arg). The PCR was carried out for 25 cycles on a Techne PHC-1 programmable heat block using 100 ng single stranded M13mp19SW0 template, with 25 pmol of VHMUT1 and the M13 primer, 0.5 mM each dNTP, 67mM Tris.HCl, pH 8.8, 10 mM MgCl₂, 17 mM (NH₄)₂SO₄, 200 µg/ml gelatine and 2.5 units Taq polymerase in a final volume of 50 µl. The temperature regime was 95°C for 1.5 min, 25°C for 1.5 min and 72°C for 3 min (However a range of PCR conditions could be used). The reaction products were extracted

with phenol/chloroform, precipitated with ethanol and resuspended in 10 mM Tris. HCl and 0.1 mM EDTA, pH 8.0.

[0167] The products from the PCR were digested with PstI and BstEII and purified on a 1.5% LGT agarose gel in Tris acetate buffer using Geneclean (Bio 101, LaJolla). The gel purified band was ligated into pSW2HPOLY (Figure 19). (This vector is related to pSW2 except that the body of the VHLYS gene has been replaced by a polylinker.) The vector was first digested with BstEII and PstI and treated with calfintestinal phosphatase. Aliquots of the reaction mix were used to transform E. coli BMH 71-18 to ampicillin resistance. Colonies were selected on ampicillin (100 µg/ml) rich plates containing glucose at 0.8% w/v.

[0168] Colonies resulting from transfection were picked in pools of five into two 96 well Corning microtitre plates, containing 200 µl 2 x TY medium and 100 µl TY medium, 100 µg/ml ampicillin and 1% glucose. The colonies were grown for 24 hours at 37°C and then cells were washed twice in 200 µl 50 mM NaCl, pelleting the cells in an IEC Centra-3 bench top centrifuge with microtitre plate head fitting. Plates were spun at 2,500 rpm for 10 min at room temperature. Cells were resuspended in 200 µl 2 x TY, 100 µg/ml ampicillin and 1 mM IPTG (Sigma) to induce expression, and grown for a further 24 hr.

[0169] Cells were spun down and the supernatants used in ELISA with lysozyme coated plates and anti-idiotypic sera (raised in rabbits against the Fv fragment of the D1.3 antibody). Bound anti-idiotypic serum was detected using horse radish peroxidase conjugated to anti-rabbit sera (ICN Immunochemicals). Seven of the wells gave a positive result in the ELISA. These pools were restreaked for single colonies which were picked, grown up, induced in microtitre plates and rescreened in the ELISA as above. Positive clones were grown up at the 50 ml scale and expression was induced. Culture supernatants were purified as in Example 5 on columns of lysozyme-Sepharose and eluates analysed on SDS-PAGE and staining with Page Blue 90 (BDH). On elution of the column with diethylamine, bands corresponding to the VHLYS mutant domains were identified, but none to the VKLYS domains. This suggested that although the mutant domains could bind to lysozyme, they could no longer associate with the VKLYS domains.

[0170] For seven clones giving a positive reaction in ELISA, plasmids were prepared and the VKLYS gene excised by cutting with EcoRI and religating. Thus the plasmids should only direct the expression of the VHLYS mutants. 1.5 ml cultures were grown and induced for expression as above. The cells were spun down and supernatant shown to bind lysozyme as above. (Alternatively the amplified mutant VKLYS genes could have been cloned directly into the pSW1HPOLY vector for expression of the mutant activities in the absence of VKLYS.)

[0171] An ELISA method was devised in which the activities of bacterial supernatants for binding of lysozyme (or KLH) were compared. Firstly a vector was devised for tagging of the VH domains at its C-terminal region with a peptide from the c-myc protein which is recognised by a monoclonal antibody 9E10. The vector was derived from pSW1 by a BstEII and SmaI double digest, and ligation of an oligonucleotide duplex made from

35 5' GTC ACC GTC TCC TCA GAA CAA AAA CTC ATC TCA GAA GAG GAT
CTG AAT TAA TAA 3' and

40 5' TTA TTA ATT CAG ATC CTC TTC TGA GAT GAG TTT TTG TTC TGA
GGA GAC G 3'.

The VHLYSMYC protein domain expressed after induction was shown to bind to lysozyme and to the 9E10 antibody by ELISA as follows:

- 45 (1) Falcon (3912) flat bottomed wells were coated with 180 µl lysozyme (3 mg/ml) or KLH (50 µg/ml) per well in 50 mM NaHCO₃, pH 9.6, and left to stand at room temperature overnight;
- 50 (2) The wells were washed with PBS and blocked for 2 hrs at 37°C with 200 µl 2% Sainsbury's instant dried skimmed milk powder in PBS per well;
- 55 (3) The Blocking solution was discarded, and the walls washed out with PBS (3 washes) and 150 µl test solution (supernatant or purified tagged domain) pipetted into each well. The sample was incubated at 37°C for 2 hrs;
- 60 (4) The test solution was discarded, and the wells washed out with PBS (3 washes). 100 µl of 4 µg/ml purified 9E10 antibody in 2% Sainsbury's instant dried skimmed milk powder in PBS was added, and incubated at 37°C for 2 hrs;
- 65 (5) The 9E10 antibody was discarded, the wells washed with PBS (3 washes). 100 µl of 1/500 dilution of anti-mouse antibody (peroxidase conjugated anti-mouse Ig (Dakopats)) was added and incubated at 37°C for 2 hrs;
- 70 (6) The second antibody was discarded and wells washed three times with PBS; and
- 75 (7) 100 µl 2,2'-azino-bis(3-ethylbenzthiazolinesulphonic acid) [Sigma] (0.55 mg/ml, with 1 µl 20% hydrogen perox-

ide: water per 10 ml) was added to each well and the colour allowed to develop for up to 10 minutes at room temperature.

5 [0172] The reaction was stopped by adding 0.05% sodium azide in 50 mM citric acid, pH 4.3. ELISA plates were read in an Titertek Multiscan plate reader.

10 [0173] The activities of the mutant supernatants were compared with VHLYS supernatant by competition with the VHLYSMYC domain for binding to lysozyme. The results show that supernatant from clone VHLYSMUT59 is more effective than wild type VHLYS supernatant in competing for VHLYSMYC. Furthermore, Western blots of SDS-PAGE aliquots of supernatant from the VHLYS and VHLYSMUT59 domain (using anti-Fv antisera) indicated comparable amounts of the two samples. Thus assuming identical amounts of VHLYS and VHLYSMUT59, the affinity of the mutant appears to be greater than that of the VHLYS domain.

15 [0174] To check the affinity of the VHLYSMUT59 domain directly, the clone was grown at the 1l scale and 200-300 µg purified on lysozyme-Sepharose as in Example 5. By fluorescence quench titration of samples of VHLYS and VHLYSMUT59, the number of binding sites for lysozyme were determined. The samples of VHLYS and VHLYSMUT59 were then compared in the competition ELISA with VHLYSMYC over two orders of magnitude. In the competition assay each microtitre well contained a constant amount of VHLYSMYC (approximately 0.6 µg VHLYSMYC). Varying amounts of VHLYS or VHLYSMUT59 (3.8 µM in lysozyme binding sites) were added (0.166 - 25 µl). The final volume and buffer concentration in all wells was constant. 9E10 (anti-myc) antibody was used to quantitate bound VHLYSMYC in each assay well. The % inhibition of VHLYSMYC binding was calculated for each addition of VHLYS or VHLYSMUT59, after subtraction of background binding. Assays were carried out in duplicate. The results indicate that VHLYSMUT59 has a higher affinity for lysozyme than VHLYS.

20 [0175] The VHLYSMUT59 gene was sequenced (after recloning into M13) and shown to be identical to the VHLYS gene except for the central residues of CDR3 (Arg-Asp-Tyr-Arg). These were replaced by Thr-Gln-Arg-Pro: (encoded by ACACAAAGGCCA).

25 [0176] A library of 2000 mutant VH clones was screened for lysozyme and also for KLH binding (toothpicking 5 colonies per well as described in Example 6). Nineteen supernatants were identified with lysozyme binding activities and four with KLH binding activities. This indicates that new specificities and improved affinities can be derived by making a random repertoire of CDR3.

30 Example 8

Construction and expression of double domain for lysozyme binding.

35 [0177] The finding that single domains have excellent binding activities should allow the construction of strings of domains (concatamers). Thus, multiple specificities could be built into the same molecule, allowing binding to different epitopes spaced apart by the distance between domain heads. Flexible linker regions could be built to space out the domains. In principle such molecules could be devised to have exceptional specificity and affinity.

40 [0178] Two copies of the cloned heavy chain variable gene of the D1.3 antibody were linked by a nucleotide sequence encoding a flexible linker

Gly-Gly-Gly-Ala-Pro-Ala-Ala-Ala-Pro-Ala-Gly-Gly-Gly-

45 (by several steps of cutting, pasting and site directed mutagenesis) to yield the plasmid pSW3 (Figure 20). The expression was driven by a lacZ promoter and the protein was secreted into the periplasm via a pelB leader sequence (as described in Example 5 for expression of pSW1 and pSW2). The protein could be purified to homogeneity on a lysozyme affinity column. On SDS polyacrylamide gels, it gave a band of the right size (molecular weight about 26,000). The protein also bound strongly to lysozyme as detected by ELISA (see Example 5) using anti-idiotypic antiserum directed against the Fv fragment of the D1.3 antibody to detect the protein. Thus, such constructs are readily made and secreted and at least one of the domains binds to lysozyme.

Example 9

Introduction of cysteine residue at C-terminal end of VHLYS

55 [0179] A cysteine residue was introduced at the C-terminus of the VHLYS domain in the vector pSW2. The cysteine was introduced by cleavage of the vector with the restriction enzymes BstI and SmaI (which excises the C-terminal portion of the J segment) and ligation of a short oligonucleotide duplex

5' GTC ACC GTC TCC TCA TGT TAA TAA 3'

and

5

5' TTA TTA ACA TGA GGA GAC G 3'.

By purification on an affinity column of lysozyme Sepharose it was shown that the VHLYS-Cys domain was expressed in association with the VKLYS variable domain, but the overall yields were much lower than the wild type Fv fragment.
10 Comparison of non-reducing and reducing SDS polyacrylamide gels of the purified Fv-Cys protein indicated that the two VH-Cys domains had become linked through the introduced cysteine residue.

Example 10

15 Linking of VH domain with enzyme

[0180] Linking of enzyme activities to VH domains should be possible by either cloning the enzyme on either the N-terminal or the C-terminal side of the VH domain. Since both partners must be active, it may be necessary to design a suitable linker (see Example 8) between the two domains. For secretion of the VH-enzyme fusion, it would be preferable to utilise an enzyme which is usually secreted. In Figure 21, there is shown the sequence of a fusion of a VH domain with alkaline phosphatase. The alkaline phosphatase gene was cloned from a plasmid carrying the *E. coli* alkaline phosphatase gene in a plasmid pEK48 [51] using the polymerase chain reaction. The gene was amplified with the primers

25 5' CAC CAC GGT CAC CGT CTC CTC ACG GAC ACC AGA AAT GCC TGT
TCT G 3' and

30 5' GCG AAA ATT CAC TCC CGG GCG CGG TTT TAT TTC 3'.

The gene was introduced into the vector pSW1 by cutting at BstEII and SmaI. The construction (Figure 21) was expressed in *E. coli* strain BMH71-18 as in Example 5 and screened for phosphatase activity using 1 mg/ml p-nitrophenylphosphate as substrate in 10mM diethanolamine and 0.5 mM MgCl₂, pH 9.5) and also on SDS polyacrylamide gels which had been Western blotted (detecting with anti-idiotypic antiserum). No evidence was found for the secretion of the linked VHLYS-alkaline phosphatase as detected by Western blots (see Example 5), or for secretion of phosphatase activity.

[0181] However when the construct was transfected into a bacterial strain BL21DE3 [52] which is deficient in proteases, a band of the correct size (as well as degraded products) was detected on the Western blots. Furthermore phosphatase activity could now be detected in the bacterial supernatant. Such activity is not present in supernatant from the strain which had not been transfected with the construct.

[0182] A variety of linker sequences could then be introduced at the BstEII site to improve the spacing between the two domains.

45

Example 11

Coexpression of VH domains with Vk repertoire

50 [0183] A repertoire of Vk genes was derived by PCR using primers as described in Example 2 from DNA prepared from mouse spleen and also from mouse spleen mRNA using the primers VK3FOR and VK2BACK and a cycle of 94°C for 1 min, 60 °C for 1 min, 72°C for 2 min. The PCR amplified DNA was fractionated on the agarose gel, the band excised and cloned into a vector which carries the VHLYS domain (from the D1.3 antibody), and a cloning site (SacI and Xhol) for cloning of the light chain variable domains with a myc tail (pSW1VHLYS-VKPOLYMYC, Figure 22).

55 [0184] Clones were screened for lysozyme binding activities as described in Examples 5 and 7 via the myc tag on the light chain variable domain, as this should permit the following kinds of Vk domains to be identified:

- (1) those which bind to lysozyme in the absence of the VHLYS domain;

(2) those which associate with the heavy chain and make no contribution to binding of lysozyme; and
 (3) those which associate with the heavy chain and also contribute to binding of lysozyme (either helping or hindering).

5 [0185] This would not identify those V_k domains which associated with the VHLYS domain and completely abolished its binding to lysozyme.

[0186] In a further experiment, the VHLYS domain was replaced by the heavy chain variable domain VH3 which had been isolated from the repertoire (see Example 6), and then the V_k domains cloned into the vector. (Note that the VH3 domain has an internal SacI site and this was first removed to allow the cloning of the V_k repertoire as SacI-Xhol fragments.)

10 [0187] By screening the supernatant using the ELISA described in Example 6, bacterial supernatants will be identified which bind lysozyme.

Example 12

15 High expression of VH domains.

[0188] By screening several clones from a VH library derived from a mouse immunised with lysozyme via a Western blot, using the 9E10 antibody directed against the peptide tag, one clone was noted with very high levels of expression 20 of the domain (estimated as 25 - 50 mg/l). The clone was sequenced to determine the nature of the sequence. The sequence proved to be closely related to that of the VHLYS domain, except with a few amino acid changes (Figure 23). The result was unexpected, and shows that a limited number of amino acid changes, perhaps even a single amino acid substitution, can cause greatly elevated levels of expression.

[0189] By making mutations of the high expressing domain at these residues, it was found that a single amino acid 25 change in the VHLYS domain(Asn 35 to His) is sufficient to cause the domain to be expressed at high levels.

CONCLUSION

[0190] It can thus be seen that the present invention enables the cloning, amplification and expression of heavy and 30 light chain variable domain encoding sequences in a much more simple manner than was previously possible. It also shows that isolated variable domains or such domains linked to effector molecules are unexpectedly useful.

[0191] It will be appreciated that the present invention has been described above by way of example only and that variations and modifications may be made by the skilled person without departing from the scope of the invention.

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35 **Claims**

1. A method of cloning sequences (target sequences) each containing a sequence encoding at least part of an immunoglobulin variable domain, which method comprises providing a sample repertoire of nucleic acid containing target sequences, and using forward and back primers in the process of copying and cloning of the target sequences for expression of a repertoire of proteins each comprising at least part of an immunoglobulin variable domain, the forward primer being specific for a sequence at or adjacent the 3' end of the sense strand of each of the target sequences, the back primer being specific for a sequence at or adjacent the 3' end of the antisense strand of each of the target sequences.
- 40 2. A method according to claim 1 which method comprises:
 - (a) providing a sample repertoire of double-stranded nucleic acid containing target sequences;
 - (b) causing the two strands of the doubled-stranded nucleic acid to be separated;
 - (c) annealing to the sample a forward and a back oligonucleotide primer, the forward primer being specific for a sequence at or adjacent the 3' end of the sense strand of each of the target sequences, the back primer being specific for a sequence at or adjacent the 3' end of the antisense strand of each of the target sequences, under conditions which allow the primers to hybridize specifically to the nucleic acid;
 - (d) treating the annealed sample with a DNA polymerase enzyme in the presence of deoxynucleoside triphosphates under conditions which cause primer extension to take place, thereby producing double-stranded nucleic acid;
 - (e) repeating steps (b) to (d), thereby producing some double-stranded DNA (product DNA) containing only the target sequences;
 - (f) cloning product DNA into expression vectors for expression of a repertoire of proteins each comprising at

least part of an immunoglobulin variable domain.

3. A method according to claim 2 wherein steps (b) to (d) are repeated a plurality of times before step (f).
5. A method according to claim 1, which comprises:
 - (a) providing a repertoire of mRNA;
 - (b) annealing to the mRNA an oligonucleotide primer specific for a sequence at or adjacent the 3' end of each of the target sequences on the sense strands, under conditions which allow the primer to hybridize specifically to the nucleic acid;
 - 10 (c) treating the primer-annealed mRNA with a polymerase enzyme in the presence of deoxynucleoside triphosphates under conditions which cause primer extension to take place, thereby producing antisense cDNA;
 - (d) annealing to the cDNA an oligonucleotide primer specific for a sequence at or adjacent the 3' end of each of the target sequences on the antisense strands, under conditions which allow the primer to hybridize specifically to the nucleic acid;
 - 15 (e) treating the primer-annealed cDNA with a polymerase enzyme in the presence of deoxynucleoside triphosphates under conditions which cause primer extension to take place, thereby producing double-stranded DNA (product DNA);
 - (f) cloning product DNA into expression vectors for expression of a repertoire of proteins each comprising at least part of an immunoglobulin variable domain.
- 20 5. A method according to claim 4 wherein, after step (e) the following steps are performed before step (f):
 - (i) causing the two strands of the product DNA to be separated;
 - (ii) annealing to the separated strands a forward and a back oligonucleotide primer, the forward primer being specific for a sequence at or adjacent the 3' end of the sense strand of each of the target sequences, the back primer being specific for a sequence at or adjacent the 3' end of the antisense strand of each of the target sequences, under conditions which allow the primers to hybridize specifically to the nucleic acid;
 - 25 (iii) treating the annealed sample with a DNA polymerase enzyme in the presence of deoxynucleoside triphosphates under conditions which cause primer extension to take place, thereby producing double-stranded nucleic acid:
- 30 6. A method according to any one of claims 1 to 5 wherein the back primer is specific for a sequence at or adjacent the 3' end of the antisense strand of the sequences which are contained in the target sequences and which each encode at least part of an immunoglobulin variable domain.
- 35 7. A method according to any one of claims 1 to 6 wherein the sample repertoire of double-stranded nucleic acid is derived from lymphocytes.
- 40 8. A method according to claim 7 wherein the lymphocytes are derived from an animal or human mounting an immune response to an antigen.
9. A method according to claim 7 wherein the lymphocytes are derived from a patient with an auto-immune disease.
- 45 10. A method according to claim 1 wherein the sample repertoire of nucleic acid is derived from rearranged immunoglobulin variable region genes.
11. A method according to claim 1 wherein the sample repertoire of nucleic acid is genomic DNA.
- 50 12. A method according to claim 1 wherein the sample repertoire of nucleic acid is derived from unrearranged immunoglobulin variable region genes.
13. A method according to any one of claims 1 to 12 wherein the target sequence contains a sequence encoding a variable domain from an immunoglobulin heavy chain.
- 55 14. A method according to claim 13 wherein the product DNA is inserted into an expression vector for expression of single domain ligands selectable by their binding affinity for antigen.

15. A method according to any one of claims 1 to 13 wherein product DNA is inserted into an expression vector for expression of antibodies or antibody fragments selectable by their binding affinity for antigen.
- 5 16. A method according to any one of claims 1 to 13 wherein the product DNA is inserted into an expression vector for expression alone.
- 10 17. The method of any one of claims 1 to 13 wherein the product DNA is inserted into an expression vector for expression in combination with a complementary variable domain.
- 15 18. A method according to any one of claims 1 to 13 wherein the product DNA is inserted into an expression vector already containing sequences encoding one or more constant domains for expression.
- 20 19. A method according to any one of claims 1 to 13 wherein the product DNA is inserted into an expression vector for expression as fusion proteins.
- 25 20. A method according to any one of claims 1 to 13 wherein the product DNA is inserted into an expression vector for expression with peptide tags.
- 30 21. A method according to any one of claims 1 to 13 wherein product DNA containing sequences encoding at least immunoglobulin heavy chain variable domains and product DNA containing sequences encoding at least immunoglobulin light chain variable domains are inserted into expression vectors for expression of a combinatorial repertoire of complementary variable domains.
- 35 22. A method according to claim 21 wherein the product DNA is inserted into an expression vector already containing sequences encoding one or more constant domains for expression.
- 40 23. A method according to claim 21 wherein product DNA is inserted into expression vectors for expression as fusion proteins.
- 45 24. A method according to claim 21 wherein the product DNA is inserted into an expression vector for expression with peptide tags.
- 50 25. A method according to any one of claims 1 to 24 wherein the forward and back primers are provided as single oligonucleotides.
- 55 26. A method according to any one of claims 1 to 24 wherein the forward primers are supplied as a mixture of oligonucleotides.
- 60 27. A method according to any one of claims 1 to 24 wherein the back primers are supplied as a mixture of oligonucleotides.
- 65 28. A method according to any one of claims 1 to 27 wherein each primer includes a sequence encoding a restriction enzyme recognition site.
- 70 29. A method according to claim 28 wherein the restriction enzyme recognition site is located in the sequence which is annealed to the nucleic acid.
- 75 30. A method according to claim 1 wherein the back primer is a general primer useful for cloning a desired antibody specificity from a specific species.
- 80 31. A method according to claim 1 wherein the back primer is a mixture of primers having a variety of sequences designed to be complementary to the various families of VH, Vk or V sequences.
- 85 32. An expression library comprising a repertoire of nucleic acid sequences for expression of a repertoire of proteins each comprising an immunoglobulin variable domain.
- 90 33. An expression library comprising a repertoire of third CDR sequences, said sequences being located in an otherwise invariant VH gene.

Patentansprüche

1. Verfahren zum Klonieren von Sequenzen (Zielsequenzen), die jeweils eine zumindest für einen Teil einer variablen Immunglobulindomäne kodierende Sequenz enthalten, wobei das Verfahren die Bereitstellung einer Probensammlung von Zielsequenzen enthaltenden Nucleinsäuren und die Verwendung von Vorwärts- und Rückwärtsprimern im Verfahren des Kopierens und Klonierens der Zielsequenz zur Expression einer Sammlung von Proteinen umfasst, von denen jedes zumindest einen Teil einer variablen Immunglobulindomäne umfasst, wobei der Vorwärtsprimer für eine Sequenz am oder benachbart zum 3'-Ende des Sense-Strangs jeder Zielsequenz spezifisch ist und der Rückwärtsprimer für eine Sequenz am oder benachbart zum 3'-Ende des Antisense-Strangs jeder Zielsequenz spezifisch ist.

5 2. Verfahren nach Anspruch 1, wobei das Verfahren Folgendes umfasst:

- (a) Breitstellung einer Probensammlung von Zielsequenzen enthaltender doppelsträngiger Nucleinsäure;
- (b) Bewirken einer Trennung der zwei Stränge der doppelsträngigen Nucleinsäure;
- (c) Anellieren eines Vorwärts- und eines Rückwärts-Oligonucleotidprimers an die Probe, wobei der Vorwärtsprimer für eine Sequenz am oder benachbart zum 3'-Ende des Sense-Strangs jeder Zielsequenz spezifisch ist und der Rückwärtsprimer für eine Sequenz am oder benachbart zum 3'-Ende des Antisense-Strangs jeder Zielsequenz spezifisch ist, unter Bedingungen, die spezifische Hybridisierung der Primer an die Nucleinsäure ermöglichen;
- (d) Behandlung der anellierten Probe mit einem DNA-Polymerase-Enzym in Gegenwart eines Desoxynucleosidtriphosphats unter Bedingungen, die eine Primerextension bewirken, wodurch doppelsträngige Nucleinsäure erzeugt wird;
- (e) Wiederholung der Schritte (b) bis (d), wodurch doppelsträngige DNA (Produkt-DNA) erzeugt wird, die nur die Zielsequenzen enthält;
- (f) Klonieren der Produkt-DNA in Expressionsvektoren zur Expression einer Sammlung von Proteinen, von denen jedes zumindest einen Teil einer variablen Immunglobulindomäne umfasst.

10 3. Verfahren nach Anspruch 2, worin die Schritte (b) bis (d) vor Schritt (f) mehrmals wiederholt werden.

15 4. Verfahren nach Anspruch 1, umfassend:

- (a) die Bereitstellung einer mRNA-Sammlung;
- (b) das Anellieren eines Oligonucleotidprimers an die mRNA, der für eine Sequenz am oder benachbart zum 3'-Ende des Sense-Strangs jeder Zielsequenz spezifisch ist, unter Bedingungen, die spezifische Hybridisierung des Primers an die Nucleinsäure ermöglichen;
- (c) die Behandlung der mRNA mit anelliertem Primer mit einem Polymerase-Enzym in Gegenwart eines Desoxynucleosidtriphosphats unter Bedingungen, die eine Primerextension bewirken, wodurch Antisense-cDNA erzeugt wird;
- (d) das Anellieren eines Oligonucleotidprimers an die cDNA, der für eine Sequenz am oder benachbart zum 3'-Ende des Antisense-Strangs jeder Zielsequenz spezifisch ist, unter Bedingungen, die spezifische Hybridisierung des Primers an die Nucleinsäure ermöglichen;
- (e) die Behandlung der cDNA mit anellierten Primer mit einem Polymerase-Enzym in Gegenwart eines Desoxynucleosidtriphosphats unter Bedingungen, die eine Primerextension bewirken, wodurch doppelsträngige DNA (Produkt-DNA) erzeugt wird;
- (f) das Klonieren der Produkt-DNA in Expressionsvektoren zur Expression einer Sammlung von Proteinen, von denen jedes zumindest einen Teil einer variablen Immunglobulindomäne umfasst.

20 5. Verfahren nach Anspruch 4, worin nach Schritt (e) und vor Schritt (f) die folgenden Schritte durchgeführt werden:

- (i) Bewirken einer Trennung der zwei Stränge der Produkt-DNA;
- (ii) Anellieren eines Vorwärts- und eines Rückwärts-Oligonucleotidprimers an die getrennten Stränge, wobei der Vorwärtsprimer für eine Sequenz am oder benachbart zum 3'-Ende des Sense-Strangs jeder Zielsequenz spezifisch ist und der Rückwärtsprimer für eine Sequenz am oder benachbart zum 3'-Ende des Antisense-Strangs jeder Zielsequenz spezifisch ist, unter Bedingungen, die spezifische Hybridisierung der Primer an die Nucleinsäure ermöglichen;
- (iii) Behandlung der anellierten Probe mit einem DNA-Polymerase-Enzym in Gegenwart eines Desoxynucleosidtriphosphats unter Bedingungen, die eine Primerextension bewirken, wodurch doppelsträngige Nucleinsäure erzeugt wird;

säure erzeugt wird.

6. Verfahren nach einem der Ansprüche 1 bis 5, worin der Rückwärtsprimer für eine Sequenz am oder benachbart zum 3'-Ende des Antisense-Strangs der Sequenzen, die in den Zielsequenzen enthalten sind und die zumindest einen Teil einer variablen Immunglobulindomäne kodieren, spezifisch ist.
5
7. Verfahren nach einem der Ansprüche 1 bis 6, worin die Sammlung doppelsträngiger Nucleinsäureproben von Lymphozyten stammen.
- 10 8. Verfahren nach Anspruch 7, worin die Lymphozyten von einem Menschen oder Tier stammen, der/das eine Immunantwort auf ein Antigen zeigt.
9. Verfahren nach Anspruch 7, worin die Lymphozyten von einem Patienten mit einer Autoimmunerkrankung stammen.
15
10. Verfahren nach Anspruch 1, worin die Nucleinsäureprobensammlung von Genen für umgeordnete variable Domänen von Immunglobulinen stammt.
11. Verfahren nach Anspruch 1, worin die Nucleinsäureprobensammlung genomische DNA ist.
20
12. Verfahren nach Anspruch 1, worin die Nucleinsäureprobensammlung von Genen für nicht umgeordnete variable Domänen von Immunglobulinen stammt.
13. Verfahren nach einem der Ansprüche 1 bis 12, worin die Zielsequenz eine Sequenz enthält, die für eine variable Domäne einer schweren Immunglobulinkette kodiert.
25
14. Verfahren nach Anspruch 13, worin die Produkt-DNA in einen Expressionsvektor zur Expression von einzelnen Domänen-Liganden eingeführt wird, die nach ihrer Bindungsaffinität für das Antigen selektierbar sind.
15. Verfahren nach einem der Ansprüche 1 bis 13, worin Produkt-DNA in einen Expressionsvektor zur Expression von Antikörpern oder Fragmenten von Antikörpern eingeführt wird, die nach ihrer Bindungsaffinität für das Antigen selektierbar sind.
30
16. Verfahren nach einem der Ansprüche 1 bis 13, worin die Produkt-DNA in einen Expressionsvektor zur alleinigen Expression eingeführt wird.
35
17. Verfahren nach einem der Ansprüche 1 bis 13, worin die Produkt-DNA in einen Expressionsvektor zur Expression in Kombination mit einer komplementären variablen Domäne eingeführt wird.
18. Verfahren nach einem der Ansprüche 1 bis 13, worin die Produkt-DNA zur Expression in einen Expressionsvektor eingeführt wird, der bereits Sequenzen enthält, die für eine oder mehrere konstante Domänen kodieren.
40
19. Verfahren nach einem der Ansprüche 1 bis 13, worin die Produkt-DNA in einen Expressionsvektor zur Expression als Fusionsproteine eingeführt wird.
45
20. Verfahren nach einem der Ansprüche 1 bis 13, worin die Produkt-DNA in einen Expressionsvektor zur Expression mit Peptidmarkierungen eingeführt wird.
21. Verfahren nach einem der Ansprüche 1 bis 13, worin Produkt-DNA, die zumindest für variable Domänen schwerer Immunglobulinketten kodierende Sequenzen enthält, und Produkt-DNA, die zumindest für variable Domänen leichter Immunglobulinketten kodierende Sequenzen enthält, in Expressionsvektoren zur Expression einer kombinatorischen Sammlung komplementärer variabler Domänen eingeführt werden.
50
22. Verfahren nach Anspruch 21, worin die Produkt-DNA zur Expression in einen Expressionsvektor eingeführt wird, der bereits Sequenzen enthält, die für eine oder mehrere konstante Domänen kodieren.
55
23. Verfahren nach Anspruch 21, worin Produkt-DNA in Expressionsvektoren zur Expression als Fusionsproteine eingeführt wird.

24. Verfahren nach Anspruch 21, worin die Produkt-DNA in einen Expressionsvektor zur Expression mit Peptidmarkierung eingeführt wird.
- 5 25. Verfahren nach einem der Ansprüche 1 bis 24, worin die Vorwärts- und Rückwärtsprimer als einzelne Oligonucleotide bereitgestellt werden.
- 10 26. Verfahren nach einem der Ansprüche 1 bis 24, worin die Vorwärtsprimer als Oligonucleotidgemische bereitgestellt werden.
- 15 27. Verfahren nach einem der Ansprüche 1 bis 24, worin die Rückwärtsprimer als Oligonucleotidgemische bereitgestellt werden.
28. Verfahren nach einem der Ansprüche 1 bis 27, worin jeder Primer eine Sequenz enthält, die für eine Restriktions-enzym-Erkennungsstelle kodiert.
- 15 29. Verfahren nach Anspruch 28, worin sich die Restriktionsenzym-Erkennungsstelle in der an die Nucleinsäure anellierten Sequenz befindet.
- 20 30. Verfahren nach Anspruch 1, worin der Rückwärtsprimer ein allgemeiner Primer ist, der zum Klonieren einer gewünschten Antikörperspezifität einer spezifischen Spezies dient.
- 25 31. Verfahren nach Anspruch 1, worin der Rückwärtsprimer ein Gemisch von Primern mit einer Vielfalt von Sequenzen ist, die so konzipiert sind, dass sie komplementär zu den verschiedenen Familien von VH-, Vk- oder V-Sequenzen sind.
32. Expressionsbibliothek, die ein Repertoire von Nucleinsäuresequenzen zur Expression eines Repertoires von Proteinen umfasst, die jeweils eine variable Immunglobulindomäne umfassen.
- 30 33. Expressionsbibliothek, die ein Repertoire an dritten CDR-Sequenzen umfasst, wobei sich die Sequenzen in einem ansonsten invarianten VH-Gen befinden.

Revendications

- 35 1. Méthode de clonage de séquences (séquences cibles), chacune contenant une séquence codant au moins une partie d'un domaine variable d'immunoglobuline, laquelle méthode consiste à produire un répertoire d'échantillons de séquences cibles contenant de l'acide nucléique et à utiliser des amores vers l'avant et vers l'arrière dans le processus de copiage et de clonage des séquences cibles pour l'expression d'un répertoire des protéines, chacune comprenant au moins une partie d'un domaine variable d'immunoglobuline, l'amorce vers l'avant étant spécifique d'une séquence à ou près de l'extrémité 3' du brin de sens de chacune des séquences cibles, l'amorce vers l'arrière étant spécifique d'une séquence à ou adjacente à l'extrémité 3' du brin anti-sens de chacune des séquences cibles.
- 40 2. Méthode selon la revendication 1, laquelle consiste à:
- 45 (a) prévoir un répertoire d'échantillons de séquences cibles contenant de l'acide nucléique à deux brins;
- (b) forcer les deux brins de l'acide nucléique à deux brins à se séparer;
- (c) recuire, sur l'échantillon, une amorce d'oligonucléotides vers l'avant et vers l'arrière, l'amorce vers l'avant étant spécifique d'une séquence à ou à proximité de l'extrémité 3' du brin de sens de chacune des séquences cibles, l'amorce vers l'arrière étant spécifique d'une séquence à ou adjacente à l'extrémité 3' du brin de l'anti-sens de chacune des séquences cibles, dans des conditions qui permettent aux amores de s'hybrider spécifiquement à l'acide nucléique;
- (d) traiter l'échantillon recuit avec une enzyme d'ADN polymérase en présence de désoxynucléoside triphosphates dans des conditions qui provoquent l'extension de l'amorce pour ainsi produire l'acide nucléique à deux brins;
- 50 (e) répéter les étapes (b) et (d) pour ainsi produire de l'ADN à deux brins (ADN produit) ne contenant que les séquences cibles;
- (f) cloner l'ADN produit dans des vecteurs d'expression pour l'expression d'un répertoire de protéines dont chacune comprend au moins une partie d'un domaine variable d'immunoglobuline.

3. Méthode selon la revendication 2, où les étapes (b) et (d) sont répétées un certain nombre de fois avant l'étape (f).
4. Méthode selon la revendication 1, qui consiste à:
 - 5 (a) produire un répertoire d'ARNm;
 - (b) recuire, sur l'ARNm, une amorce d'oligonucléotides spécifique d'une séquence à ou adjacente à l'extrémité 3' de chacune des séquences cibles sur les brins de sens, dans des conditions qui permettent à l'amorce de s'hybrider spécifiquement à l'acide nucléique;
 - 10 (c) traiter l'ARNm recuit à l'amorce par une enzyme polymérase en présence de désoxynucléoside triphosphates dans des conditions qui provoquent l'extension de l'amorce pour ainsi produire l'ADNc anti-sens;
 - (d) recuire, à l'ADNc, une amorce d'oligonucléotides spécifique d'une séquence à ou adjacente à l'extrémité 3' de chacune des séquences cibles sur les brins anti -sens, dans des conditions qui permettent à l'amorce de s'hybrider spécifiquement à l'acide nucléique;
 - 15 (e) traiter l'ADNc recuit à l'amorce par une enzyme polymérase en présence de désoxynucléoside triphosphates dans des conditions qui provoquent l'extension de l'amorce, pour ainsi produire de l'ADN à deux brins (ADN produit);
 - (f) cloner l'ADN produit dans des vecteurs d'expression pour l'expression d'un répertoire de protéines, chacune comprenant au moins une partie d'un domaine variable d'immunoglobuline.
- 20 5. Méthode selon la revendication 4 où, après l'étape (e), on accomplit, avant l'étape (f), les étapes suivantes:
 - (i) provoquer la séparation des deux brins de l'ADN produit;
 - (ii) recuire, aux brins séparés, une amorce d'oligonucléotides vers l'avant et vers l'arrière, l'amorce vers l'avant étant spécifique d'une séquence à ou adjacente à l'extrémité 3' du brin de sens de chacune des séquences cibles, l'amorce vers l'arrière étant spécifique d'une séquence à ou adjacente à l'extrémité 3' du brin d'anti-sens de chacune des séquences cibles, dans des conditions qui permettent aux amorces de s'hybrider spécifiquement à l'acide nucléique;
 - 25 (iii) traiter l'échantillon recuit avec une enzyme d'ADN polymérase en présence de désoxynucléoside triphosphates dans des conditions qui provoquent une extension de l'amorce pour ainsi produire l'acide nucléique à deux brins.
6. Méthode selon l'une quelconque des revendications 1 à 5, où l'amorce vers l'arrière est spécifique d'une séquence à ou adjacente à l'extrémité 3' du brin d'anti-sens des séquences qui sont contenues dans les séquences cibles et dont chacune code au moins une partie d'un domaine variable d'immunoglobuline.
- 35 7. Méthode selon l'une quelconque des revendications de 1 à 6, où le répertoire d'échantillons de l'acide nucléique à deux brins est dérivé de lymphocytes.
8. Méthode selon la revendication 7, où les lymphocytes sont dérivés d'un animal ou humain montrant une réponse immunitaire à un antigène.
- 40 9. Méthode selon la revendication 7, où les lymphocytes sont dérivés d'un patient présentant une maladie autoimmune.
- 45 10. Méthode selon la revendication 1, où le répertoire d'échantillons de l'acide nucléique est dérivé de gènes de régions variables d'immunoglobuline qui sont réarrangées.
11. Méthode selon la revendication 1, où le répertoire d'échantillons de l'acide nucléique est l'ADN génomique.
- 50 12. Méthode selon la revendication 1, où le répertoire d'échantillons de l'acide nucléique est dérivé de gènes de régions variables d'immunoglobuline qui ne sont pas réarrangées.
13. Méthode selon l'une quelconque des revendications 1 à 12, où la séquence cible contient une séquence codant un domaine variable d'une chaîne lourde d'immunoglobuline.
- 55 14. Méthode selon la revendication 13, où l'ADN produit est inséré dans un vecteur d'expression pour l'expression de ligands de domaine simple pouvant être sélectionnés par leur affinité de liaison pour l'antigène.

15. Méthode selon l'une quelconque des revendications 1 à 13, où l'ADN produit est inséré dans un vecteur d'expression pour l'expression des anticorps ou des fragments d'anticorps pouvant être sélectionnés par leur affinité de liaison pour l'antigène.
- 5 16. Méthode selon l'une quelconque des revendications 1 à 13, où l'ADN produit est inséré dans un vecteur d'expression pour l'expression seule.
- 10 17. Méthode selon l'une quelconque des revendications 1 à 13, où l'ADN produit est inséré dans un vecteur d'expression pour l'expression en combinaison avec un domaine variable complémentaire.
18. Méthode selon l'une quelconque des revendications 1 à 13, où l'ADN produit est inséré dans un vecteur d'expression contenant déjà des séquences codant un ou plusieurs domaines constants pour l'expression.
- 15 19. Méthode selon l'une quelconque des revendications 1 à 13, où l'ADN produit est inséré dans un vecteur d'expression pour l'expression en tant que protéines de fusion.
- 20 20. Méthode selon l'une quelconque des revendications 1 à 13, où l'ADN produit est inséré dans un vecteur d'expression pour l'expression avec des marqueurs de peptides.
21. Méthode selon l'une quelconque des revendications 1 à 13, où l'ADN produit contenant des séquences codant au moins des domaines variables de chaîne lourde d'immunoglobuline et l'ADN produit contenant des séquences codant au moins des domaines variables de chaîne légère d'immunoglobuline sont insérés dans des vecteurs d'expression pour l'expression d'un répertoire en combinaison de domaines variables complémentaires.
- 25 22. Méthode selon la revendication 21, où l'ADN produit est inséré dans un vecteur d'expression contenant déjà des séquences codant un ou plusieurs domaines constants pour l'expression.
23. Méthode selon la revendication 21, où l'ADN produit est inséré dans des vecteurs d'expression pour l'expression en tant que protéines de fusion.
- 30 24. Méthode selon la revendication 21, où l'ADN produit est inséré dans un vecteur d'expression pour l'expression avec des marqueurs de peptides.
25. Méthode selon l'une quelconque des revendications 1 à 24, où les amores vers l'avant et vers l'arrière sont produites sous la forme d'oligonucléotides simples.
- 35 26. Méthode selon l'une quelconque des revendications 1 à 24, où les amores vers l'avant sont fournies sous la forme d'un mélange d'oligonucléotides.
27. Méthode selon l'une quelconque des revendications 1 à 24, où les amores vers l'arrière sont fournies sous la forme d'un mélange d'oligonucléotides.
- 40 28. Méthode selon l'une quelconque des revendications 1 à 27, où chaque amorce contient une séquence codant un site de reconnaissance d'une enzyme de restriction.
29. Méthode selon la revendication 28, où le site de reconnaissance d'une enzyme de restriction est placé dans la séquence qui est recuite à l'acide nucléique.
- 45 30. Méthode selon la revendication 1, où l'amorce vers l'arrière est une amorce générale utile pour cloner une spécificité d'anticorps souhaité d'une espèce spécifique.
31. Méthode selon la revendication 1, où l'amorce vers l'arrière est un mélange d'amores ayant une variété de séquences désignées pour être complémentaires aux diverses familles des séquences VH, Vk ou V.
- 50 32. Bibliothèque d'expression comprenant un répertoire d'acides nucléiques pour l'expression d'un répertoire de protéines, chacune comprenant un domaine variable d'immunoglobuline.
33. Bibliothèque d'expression comprenant un répertoire de troisièmes séquences de CDR, lesdites séquences étant

placées dans un gène VH autrement invariant.

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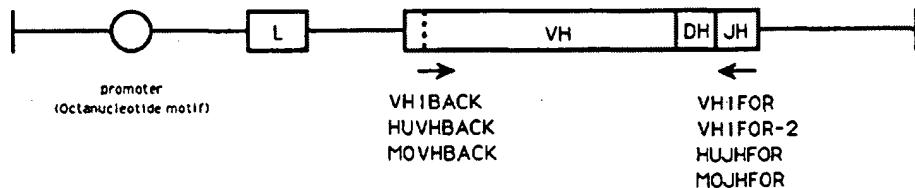
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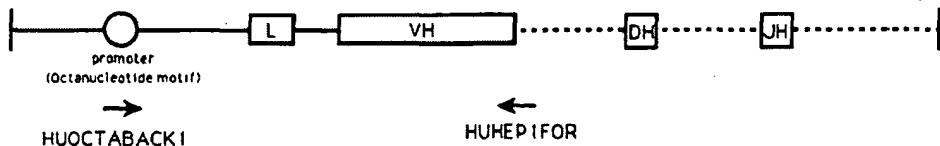
50

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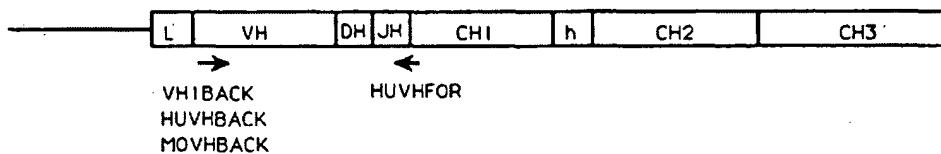
Rearranged heavy chain variable gene (DNA)



Unrearranged heavy chain variable gene (DNA)



Rearranged heavy chain variable gene (mRNA)



Rearranged light chain variable gene (DNA)

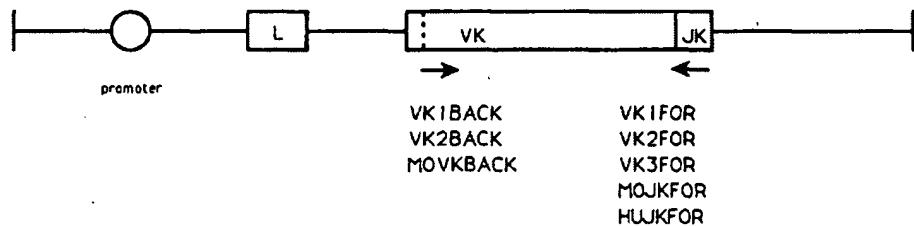


FIG. 1

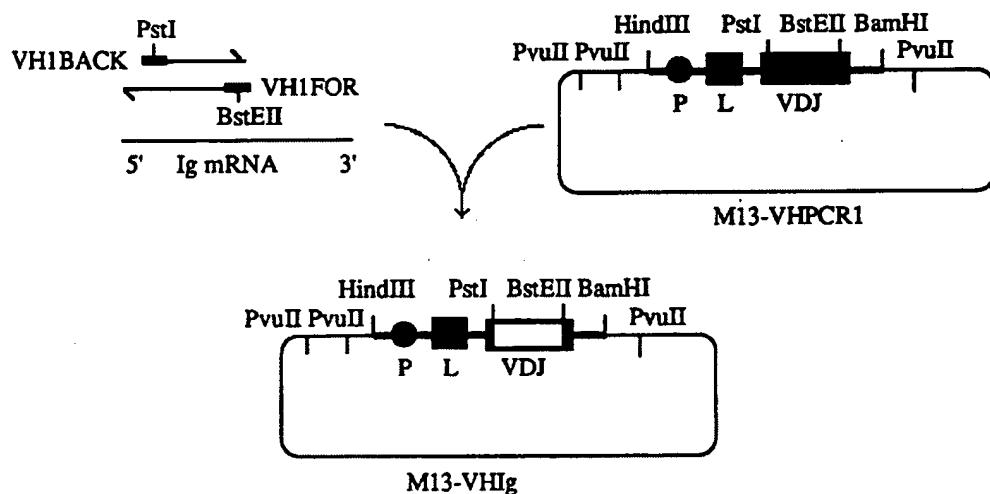


FIG. 2

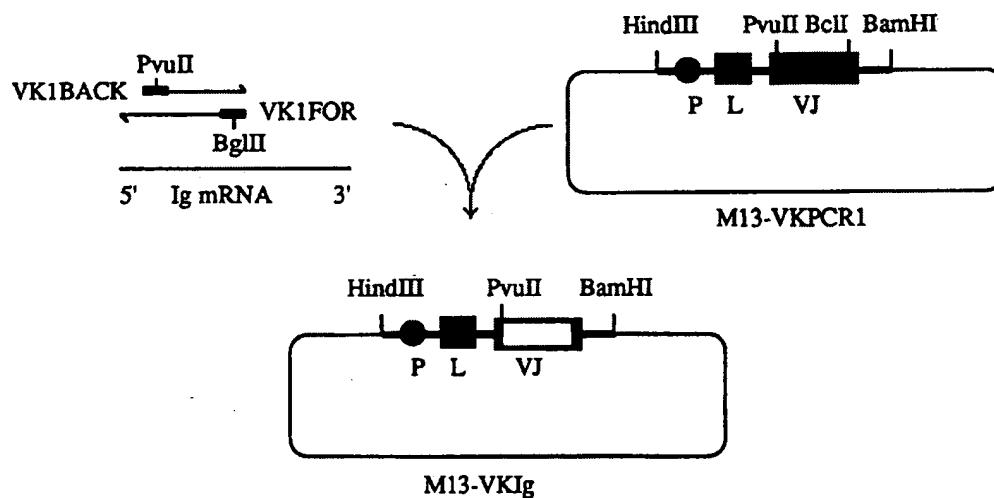


FIG. 4

M13 VHPCR1Hind III^(a)

AAGCTTATGAATATGCAAATCCTCTGAATCTACATGGAAATATAGGTTGTCTATACCA
 10 20 30 40 50 60
 CAAACAGAAAAACATGAGATCACAGTTCTCTACAGTTACTGAGCACACAGGACCTCAC
 70 80 90 100 110 120

M G W S C I I L F L V A T A T
 CATGGGATGGAGCTGTATCATCCTCTTGGTAGCAACAGCTACAGGTAGGGGCTCAC
 130 140 150 160 170 180

AGTAGCCAGGCTTGAGGTCTGGACATATATATGGGTGACAATGACATCCACTTGCCTTC
 190 200 210 220 230 240

PstI

G V H S Q V Q L Q E S G P G L V R P
 1 5 10
 TCTCCACAGGTGTCCACTCCCAGGTCCA
 250 260 270 280 290 300

CDR1

S Q T L S L T C T V S G S T F S S Y W M
 CTAGCCAGACCCCTGAGGCTGACCTTGACCGTGTCTGGCAGCACCTTCAGCAGCTACTGGA
 310 320 330 340 350 360

CDR2

H W V R Q P P G R G L E W I G R I D P N
 TGCACTGGGTGAGACAGCCACCTGGACGGTCTTGAGTGGATTGAAAGGATTGATCCTA
 370 380 390 400 410 420

S G G T K Y N E K F K S R V T M L V D T
 ATAGTGGTGGTACTAAGTACAATGAGAGTTCAAGAGCAGACTGACAATGCTGGTAGACA
 430 440 450 460 470 480

S K N Q F S L R L S S V T A A D T A V Y
 CCAGCAAGAACCAAGTCAGCCTGAGACTCAGCAGCGTACAGCGCCGACACCGCGGTCT
 490 500 510 520 530 540

CDR3

Y C A R Y D Y Y G S S Y F D Y W G Q G T
 ATTATTGTGCAAGATACTGATTACTACGTTAGTAGCTACTTGTACTACTGGGCCAAGGGA
 550 560 570 580 590 600

BstEII

T V T V S S
 CCACGGTCACCGTCTCCTCAGGTGAGTCCTTACAACCTCTCTCTTCTATTCAAGCTAAAT
 610 620 630 640 650 660

AGATTTTACTGCATTGTTGGGGGGAAATGTTGTATCTGAATTTCAGGTATGAAGGA
 670 680 690 700 710 720

CTAGGGACACCTTGGGAGTCAGAAAGGGTCAATTGGGAGCCGGCTGATGCAGACAGACA
 730 740 750 760 770 780

BamHI

TCCTCAGCTCCCAGACTTCATGGCCAGAGATTATAG
 790 800 810

FIG. 3

M1.3 VκPCR1

HinD III

AAGCTTATGAAATGCAAATCCCTCTGAATCTACATGGTAAATATAGGTTGTCTATACCA
 38 48 58 68 78 88

CAAAACAGAAAAACATGAGATCACAGTTCTCTACAGTACTGAGCACACAGGACCTCAC
 98 108 118 128 138 148

M G W S C I I L F L V A T A T
 CATGGATGGAGCTGTATCATCCTCTTGTGAGCAACAGCTACAGGTAAAGGGCTCAC
 158 168 178 188 198 208

AGTAGCAGGCTTGAGGTCTGGACATATATATGGGTGACATGACATCCACTTGCCTTC
 218 228 238 248 258 268

Pvu II

G V H S D I Q L T Q S P S S L S A S
 1 5 10
 TCTCCACAGGTGTCCACTCGACATCCAGCTGACCCAGAGGCCAAGCAGGCCCTGAGGCCA
 278 288 298 308 318 328

CDR1

15 20 25 30
 V G D R V T I T C R A S G N I H N Y L A
 GCGTGGGTGACAGAGTGACCATCACCTGTAGAGCCAGGGTAACATCCACAACCTACCTGG
 338 348 358 368 378 388

CDR2

35 40 45 50
 W Y Q Q K P G K A P K L L I Y Y T T T T L
 CTTGGTACCAGCAGAACCGAGGTAAAGGCTCCAAAGCTGCTGATCTACTACACCACCC
 398 408 418 428 438 448

55 60 65 70
 A D G V P S R F S G S G S G T D F T F T
 TGCTGACCGTGTGCCAACGCAAGATTCAAGCGGTAGCGGTACCGACTTCACCTICA
 458 468 478 488 498 508

CDR3

75 80 85 90
 I S S L Q P E D I A T Y Y C Q H F W S T
 CCATCAGCAGCCCTCCAGGCAAGGACATGCCACCTACTACTGCCAGCACITCTGGAGCA
 518 528 538 548 558 568

Bcl I (requires *dam*⁻ host)

95 100 105 108
 P R T F G Q G T K V V I K R
 CCCAAGGACGTTGGCCAAGGGACCAAGGTGGTGATCAAACGTGAGTAGAATTAACT
 578 588 598 608 618 628

BamHI

TTGCTTCCTCAGTTGGATCC
 638 648

FIG. 5

Sequence of MBr1 VH

Splice -1
↓ G V H S
AGGTGTCCACTCC

1 PstI	10	20
Q V Q L Q E S G T E L A S P G A S V T L		
<u>CAGGTCCA</u> CTGCAGGAGTCAGGA <u>ACTGAGCTGGCGAGTCC</u> TGGGCA <u>TCA</u> GACACTG		
VH1BACK SITE		
30 CDR1	40	
S C K A S' G Y T F T [D H I I N] W V K K R		
TCCTGCAAGGCTCTGGCTACACATTACTGACCATAATTAAAATGGTAAAAAGAGG		
52a 53 CDR2		
P G Q G L E W I G [R I Y P V S G V T N Y]		
CCTGGACAGGGCCTGAGTGGATTGGAAGGATTATCCAGTAAGTGGTGA <u>ACTA</u> ACTAC		
60 CDR2 65 70		
N Q K F M G K A T F S V D R S S N T V Y		
AATCAAAAATT <u>CATGGG</u> CAAGGCCACATTCTCTGTAGACCGGTCTCCA <u>ACACAGTG</u> TAC		
80 82A B C 83 90 CDR3		
M V L N S L T S E D P A V Y Y C G R [G F]		
ATGGTGTGAA <u>CTGACAT</u> CTGAGGACCTGCTGTCTATTACTGTGGAAAGGGCTT		
CDR3 103 BstEII Splice		
[D F D Y] W G Q G T T V T V S S ↓		
GATTTGACTACTGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGT.....		
VH1FOR SITE		

Sequence of MBr1 VK

Splice -1
↓ G V H S
AGGTGTCCACTCC

1 PvuII	10	20
D I Q L T Q S P P S L T V S V G E R V T		
<u>GACATT</u> CAGCTGACCCAGTC <u>CCACC</u> ATCC <u>CTGACTG</u> TGCA <u>GTAG</u> TGGAGAGAGGGTCACT		
VK1BACK SITE		
27A B C D E F CDR1		
I S C K S N Q N L L W S G N R R Y C L G		
ATCAGTTGCAAT <u>CCAAT</u> CAGAA <u>CTTT</u> TGGAGTGGAA <u>ACCG</u> GAAGGT <u>ACTG</u> TTGGC		
35 40 50 CDR2		
W H Q W K P G Q T P T P L I T [W T S D R]		
TGGCAC <u>AGTGG</u> AA <u>CCAGGG</u> CAA <u>ACTC</u> CTAC <u>ACCG</u> TGAT <u>CACCTGG</u> AC <u>ATCTG</u> ATGG		
60 60 70		
[F S] G V P D R F I G S G S V T D F T L T		
TTCTCTGGAGTCCCTGAT <u>CGTT</u> CATAGG <u>CAGTGG</u> AT <u>CTGT</u> GACAG <u>ATT</u> CA <u>CTG</u> ACC		
80 80 90 CDR3		
I S S V Q A E D V A V Y F C Q [Q H L D L]		
ATCAGCAGTGTGCA <u>GGCT</u> GAAGAT <u>GTGG</u> AG <u>TTT</u> AT <u>TTCTG</u> T <u>CA</u> G <u>CAAC</u> AT <u>TTGG</u> AC <u>CTT</u>		
95 100 BgIII/BcII Splice		
P Y T F G G G T K L E I K ↓		
CCGTACACGTT <u>GGGAGGGGG</u> ACCA <u>AGCTGG</u> GAG <u>ATCAA</u> AC <u>GTGAG</u>		
VK1FOR SITE		

FIG. 6

α -Lys 30

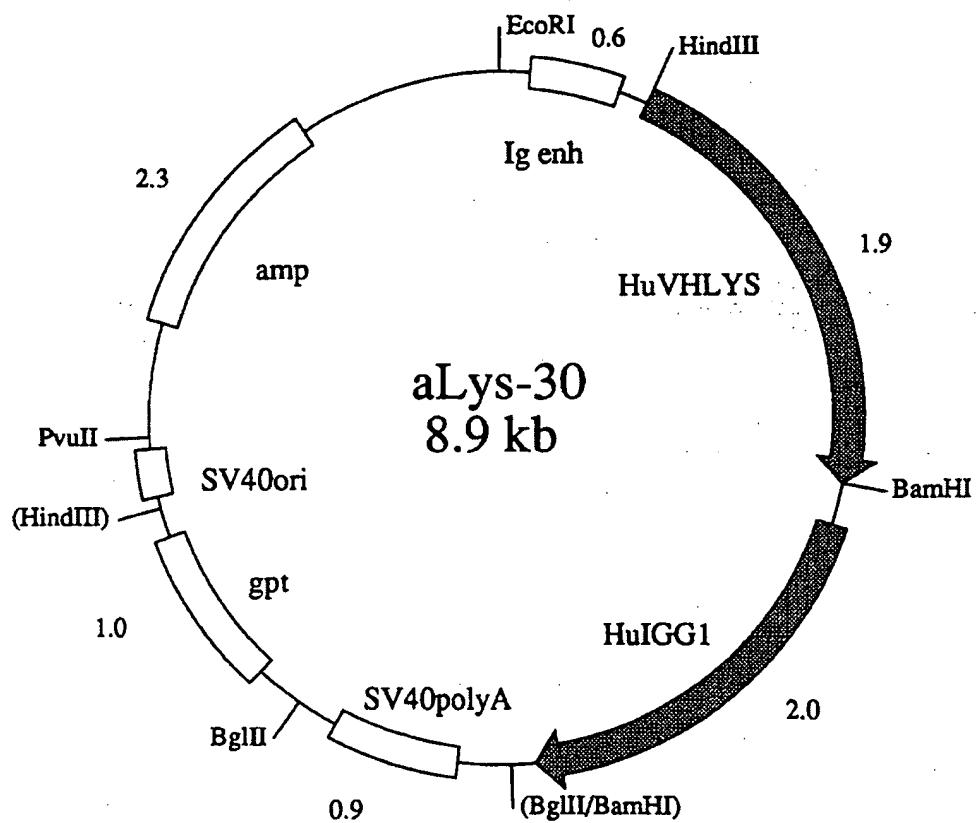


FIG. 7

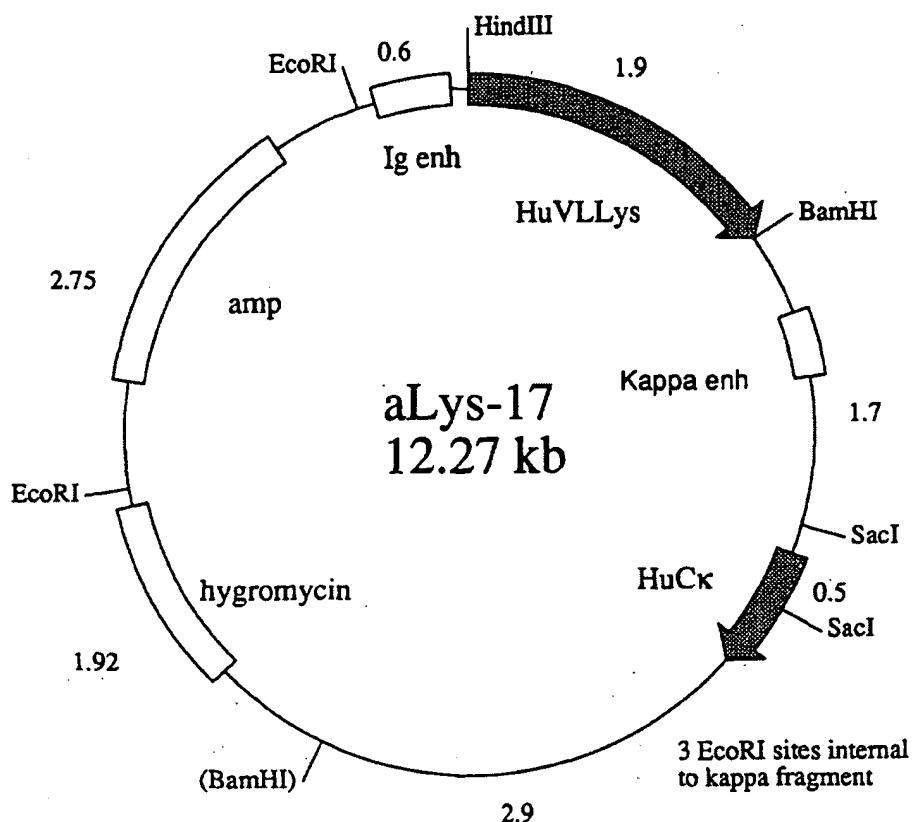
α -Lys 17

FIG. 8

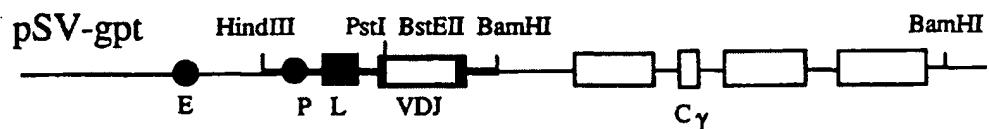
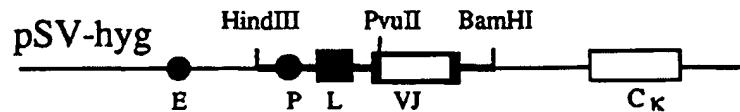


FIG. 9



	<u>F.R.1</u>	<u>CDR 1</u>	<u>CDR 2</u>	<u>CDR 3</u>
KABAT IA				
A07	PGLVKPSQSLSLTCVSGYTSIT	SGYWN	WIRQPGNKLWLG	YISYDGSSNNYNPSLKN
A09	PGLVKPSQSLFLTCVSGFPT	SGYWI	WIRQSPGKLEWLG	YITHSGETTYNPQLS
E03	PGLVKPSQSLSLTCVSGYTSIT	SGYWN	WIRQPGNKLWLG	YISYDGSSNNYNPSLKN
G01	PGLVKPSQSLSLTCVSGYTSIT	SGYWN	WIRQPGNKLWLG	YISYDGSSNNYNPSLKN
KABAT IB				
A06	PVLVAPSQSLSLTCAVSDFLST	NYGVL	WVRQPPGKGLEWLWLG	VIWAGGITNYNSALMS
25G07	PGLVQPSQSLSLTCVSGFSLT	SYGVH	WVRQSPGKGLEWLWLG	VINSGGSTDYNAAFIS
B03	PGLVAPSQSLSLTCVSGFSLT	SYGVD	WVRQPPGKGLEWLWLG	VINGGGSTNYNSALMS
G03	PGLVQPSQSLSLTCVSGFSLT	SYGVH	WVRQSPGKGLEWLWLG	VINSGGSTDYNAAFIS
H09	PVLVAPPQSLSLTCVSGFSLT	SYGVH	WVRQPPGKGLEWLWLG	VIWAGGSTNYNSALMS
25C10	PGLVAPSQSLSLTCVSGFSLT	SYAIS	WVRQPPGKGLEWLWLG	VIWAGGTNYNSALKS
A12	PGLVAPSQSLSLTCVSGFSLT	SYAIS	WVRQPPGKGLEWLWLG	VIWAGGTNYNSALKS
A08	PGLVAPSQSLSLTCVSGFSLT	SYGVH	WVRQPPGKGLEW**	*****GSTTYNSALKS
25G08	PGLVAPSQSLSLTCVSGFSLT	SYDVD	WVRQSPGKGLEWLWLG	VIWGGGSTNYNSALKS
A03	PGLVQPSQSLSLTCVSGFSLT	SYGVH	WVRQSPGKGLEWLWLG	VINSGGSTDYNAAFIS
C07	PVLVAPSQSLSLTCVSGFSLT	SYGVH	WVRQPPGKGLEWLWLG	VIWAGGSTNYNSALMS
H04	PGLVAPSQSLSLTCVSGFSLT	SYGVD	WVRQSPGKGLEWLWLG	VIWVGGSTNYNSALKS
KABAT IIA				
E04	PELVRPGVSVKISCKGSGYFTFT	DYAMH	WVKOSHAKSLEWIG	VISTYYGDASYNOKFKD
H07	PELVRPGVSVKISCKGSGYFTFT	DYAMH	WVKQSHAKSLEWIG	VISTYYGDASYNQFKD
KABAT IIB				
A02	AELVMPGASVKLSLCKASGYFTFT	SYWMH	WVKQRPQGQGLEWLWIG	EIDPDSYTNYNOKFKG
B04	AELVKPGASVLMSCSKASGYFTFT	SYWIT	WVKQRPQGQGLEWLWIG	DIYPGSGSTNYNEKFKS
C05	AELVKPGASVKLSLCKASGYFTFT	SYMMH	WVKQRPQGQGLEWLWIG	RIDPNSCGTTKYNEKFKS
C09	AELVKPGASVKLSLCKASGYFTFT	SYMMH	WVKQRPQGQGLEWLWIG	EINPSNGGTNYDEKFKS
D06	AELVKPGASVLMSCSKASGYFTFT	SYWIT	WVKQRPQGQGLEWLWIG	DIYPGSGSTNYNEKFKS
D08	PELVKPGASVLMSCSKASGYFTFT	SYMMH	WVKQRPQGQGLEWLWIG	EINPSNGGTNYNEKFKS
E07	AELVRPGASVKLSLCKASGYFTFT	DYEMH	WVKQTPVIGLEWLWIG	AIDPTEGTTAYNOKFKG
G08	PELVKPGASVKLISCKASGYFTFT	DYYIN	WVKQRPQGQGLEWLWIG	WIYPGSGNTKYNEKFKG
G10	AELVKPGASVRSVCKASGYFTFT	SYWMH	WVKQRPQGQGLEWLWIG	RIHPSDSDTNYNOKFKG
25G09	AELVKPGASVLMSCSKASGYFTFT	TYPIE	WVKONHGKSLEWIG	NFHPyNNDTKYNEKFKG
F04	TELVKPGASVKLSLCKASGYFTFT	SYMMH	WVKQRPQGQGLEWLWIG	NINPSNGGTNYNOKFKG
H02	AELVKPGASVLMSCSKASGYFTFT	SYMMH	WVKQRPQGQGLEWLWIG	NIDPSDSETHYNEKFKD
H01	AELVMPGASVKLSLCKASGYFTFT	SYMMH	WVKQRPQGQGLEWLWIG	EIDPDSYTNYN*KVQG
25C05	PELVRPGTSVRMSCSKASGYFTFF	NYWMK	WV*ORPGQGLEWLWIG	OIFFPAGSIYNNENHHD
B01	AELVKPGASVLMSCSKASGYFTFT	SYWIT	WVKQRPQGQGLEWLWIG	DIYPGSGSTNYNEKFKS
B05	AELVRPGGSVKLSLCKDSYFAFM	RHAMH	WVKQRPQGQGLEWLWIG	SFTMYSDATESENFKG
B11	AELVKPGASVLMSCSKASGYFTFT	SYWIT	WVKQRPQGQGLEWLWIG	DIYPGSGSTNYNEKFKS
KABAT III A				
25G05	GGLVQAWGSLSLSCAASGFTFT	DYYMS	WVRQPPGKALEWLWIG	FIRNKANGYtteysasvkg
C10	GGLVQPGGSLSLSCAASGFTFT	DYYMN	WVRQPPGKALEWLA	LIRHKANGYtmeysasvkg
B07	GGLVQPGGSLSLSCAASGFTFT	DYYMS	WVRQPPGKALEWLA	LIRNKANGYtteysasvkg
KABAT III B				
G05	GGLVKPGGSLSLCKSCAASGFTFS	DYGMH	WVRQAPEKGLEWVA	YISSGSSTIYYADTVKG
B12	GGLVQPGESLKLSCSESNEYEF	SHDMS	WVR*****VA	AISDGGSTYYPDPMER
D04	GGLVQPGESLRLSCAESNEYEF	SYAMS	WVA*APGKGLEWVS	AISCGGGSTYYADSVKG
D05	GGLVQPGESLRLSCAESNEYEF	SYAMS	WVA*APGKGLEWVS	AISCGGGSTYYADSVKG
F12	GGLVQPGESWKLSCVIQQ****	****	WVRQ*PEKRLEWVA	AISDGGSTYYPDPMER
F06	GGLVQPGESLRLSCAESNEYEF	SYAMS	WVA*APGKGLEWVS	AISCGGGSTYYADSAKG
D02	GGLVQPGESLKLSCSESNEYVIP	*HDMH	WVRQDSGE*LELVA	AISDGGSTYYPDPMER
F09	GDLVKPGGSLSLCKSCAASGFTFS	SYGMS	WVRQTPDKRLEWVA	TISSGGSYTYPDSVKG
KABAT III C				
E06	GGLVQPGGSMKLSCAASGFTFS	DAWMD	WVRQSPEKGLEWVA	EIRNKANNHATYYAESVKG
KABAT V A				
C04	AELVKPGASVKLSCASGYFTFT	EYTIIH	WVKQRGQGLEWIG	WFYPGSGSIKYNEKFKD

FIG. 10a

ER 3

CDR 3

RISITRDTSKNQFFLKLNSVTTEDTATYYCAR	EGNWDGFAY
PISITRETTSKNOFFQLQLNSVTTEDTATYYCAG	DRDRLGPWFAY
RISITRDTSKNQFFLKLNSVTTEDTATYYCAR	DSSGEMDY
RISITRDTSKNQFFLKLNSVTTEDTATYYCAR	VSSGYEMDY

RLSISKDTSKSVFLLKMNSLQTTDATTAYYCAR	MGDSSGYFDY	
RLSISKDTSKSVFLLKMNSLQADDTAIYYCAR	NDGYY	
RLSISKDTSKSVFLLKMNSLQTTDTAMYCAR	LGRGYAMDY	
RLSISKDTSKSVFLLKMNSLQADDTAIYYCAR	KRDYDYDRGYYYAMDY	
RLSISKDTSKSVFLLKMNSLQTTDTAMYCAI	YDGSSFFAY	
RLSISKDTSKSVFLLKMNSLQTTDTARYCAR	EGYYYPAY	
RLSISKDTSKSVFLLKMNSLQTTDARYCAR	IYYDGSSYYAMDY	
RLSISKDTSKSVFLLKMNSLQTTDTAMYCAR	13 nt.	Ps.gene/Unproductiv
RLSISKDTSKSVFLLKMNSLQTTDTAMYCAR	21 nt.	Unproductive
RLSISKDTSKSVFLLKMNSLQTTDTAMYCAR	28 nt.	Unproductive
RLSISKDTSKSVFLLKMNSLQTTDTAMYCAR	37 nt.	Unproductive
RLSISKDTSKSVFLLKMNSLQTTDTAMYCAS	32 nt.	Unproductive

KATMTVDKSSSTAYMELARLTSEDAVYYCAR 40 nt. Unproductive
 KATMTVDKSSSTAYMELARLTSEDAVYYCAR 22 nt. Unproductive

KATLTVDKSSSTAYMQLSSLTSEDSAVYYCVR	RGLTYAMDY
KATLTVDTSSTAYMQLSSLTSEDSAVYYCAR	YYSNYFDY
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR	PNWDHYYGMDV
KATLTVDTSSTAYMQLSSLTSEDSAVYYCTL	LYYYAMDY
KATLTVDTSSTAYMQLSSLTSEDSAVYYCAR	SSGYDY
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCTI	GAARATNAY
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR	GGFAY
KATLTVDTSSTAYMQLSSLTSEDSAVYYCAR	SPMDY
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAI	EVPGGFYATDY
KATLTVEKSSSTAYLESLRLSTSDDSAVYYCAR	MDYGSSLWFAY
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAK	TTVAFDY
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR	KRDYSTYFDH
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAP	TGTEFAY
KAAWAVDTSSSTAYMQLSSLTSEDTAVYFCI*	24 nt.
KATLTVDKPSDTAYMQLSSLTSEDSAVYYCAR	9 nt.
KATLTANTSSSTAYMELSSLTSEDSAVYYCAR	23 nt.
KATLTVDTSSTSYMQLSSLTSEDSAVYYCAR	15 nt.

RFTISRDNQSILYLOMNLRAEDSATYYCAR YMIGLAMDY
 RFTISRDNQSILYLOMNLRAEDSATYYCAR GYYDGSYYAMDY
 RFTISRDNQSILYLOMNLRAEDSATYYCAR 23 nt. Unproductive

RFT1SRDNNAKNTLFLQMTSLRSEDTAMYCAR	AKFHLYFDY	
RFT1SRDNTKTLYLQMSSLRSEDTALYYCAR	REGVVESRLDGV	Ps. gene
RFT1SRDNSKNTLYLQMNSLRRAEDTAVYYCAR	RGLHWFDP	Ps. gene
RFT1SRDNSKNTLYLQMNSLRRAEDTAVYYCAR	RNYGSSPFDY	Ps. gene
RFT1SRDNSKTLYLQMSSLRSEDTALYYCAR	PPMPSY	Ps. gene
RFT1SRDNTKTLYLQMNSLRRAEDTAVYYCAR	43 nt.	Ps. gene/Unproductive
RFT1SRDNTKTLYLQMSSLRSEDTALYYCAR	28 nt.	Ps. gene/Unproductive
RFT1SRDNNAKNTLYLQMSSLKSEDTAMYCAR	35 nt.	Unproductive

RFTISRDDSKSRVYLMNSLRAEDTGIYYCTG 30 nt. Unproductive

KATLTADKSSSTVYMELSLTSEDSAVYFCAR HEDRDSSGYAMDY

FIG. 10b

CDR_2FRAMEWORK_3CDR_3

KABAT HUMAN VH1

HAQKFQG	STSTAYMELSLRSEDTAVYCAR	GEGWDHF DY
GYAQKFQG	RVTIRRHKSTSTAYMELSSLRSEDTAVYCAR	GSRYGYDCSGYYL
	RVTMTRNTSISTATMELSSLRSEDTAVYCAR	LAHFSGSPVDFDP

KABAT HUMAN VH2

KHQLQPSLK S	RVTISVDTSKNQFSLKLSVTAADTAVYCAR	GGVVPAAIMDV
KS	RVTISVDTSKNQFSLKLSVTAADTAVYCAR	MARYYDFWSGYSAYYDY
SLKS	RLSISQDTSRNQFSLRLLSSVTAADTAVYCAR	HRNWGSPVHF DY
	ESTSTAYMELSSLRSEDTAVYCAR	DSYGDYGGHY

KABAT HUMAN VH3

ISYITSSSYNYADSVKG	RFTISRDNAKNSLYLQMNSLRADDTAVYCAR	DGRFGTYSPSDY
SVKG	RFTISRDDSKSIAYLQVNSLKTEDTAVYCTR	TIYYDSSGYPYW
YADSVKG	RFTISRDNAKNSLFIQMSSLRAEDTAVYCAR	GIALDAFDI
YYADSVRD	RFTISRDNSKNTLYLQMNSLRAEDTAVYCAK	53 NT. UNPROD REARR
DSVKG	RFTISRDNAKNSLYLQMNSLRDEDTAVYCAR	DHSGTGGGGGSYF
VSAISGGSTYYADSVKG	RFTISRDNPKNTLYLQMNSLRSEDTAVYCAR	KDNLWFD P
AVISYDGSKYYADSVKG	RFTISRDNSKNTLYLQMNSLRAEDTAVYCAR	DLGGRGVVVVPAPGGRS1YYYGMDV
GAVISYDGSKYYADSVKG	RFTISRDNSKNTLYLQMNSLRAEDTAVYCAS	LEGIGTIYYGMDV
QYAASVKG	AKNSLYLQMNSLRAEDTAVYCVR	DDSSSWPKHFQH
	RFTISRDDSKNSLYLQMNSLNTEDTAVYCVR	SGVVPYLDY

KNOWN FAMILY

AVYCAR	DPRIAARPDY YYYYMDV
TAMYCAR	GAEVVEPTARYYYGLNV

FIG. 11

FR1	CDR1	FR2
YTF	SYGIS	WVTTGPWTRDLRWMG
GEKPGSSVKVSCKASGYTFT	DYFMN	WMRQAPGQRLEWMG
QVQLQEIGPRTGEASETLSLICAVSGDSIS	SGNW*I	WVRQPPGKGLEWIG
QVQLQESGPGLVK*SETSLTCTVSGGSIS	SYWS	WIRQPPGKGLEWIG
GYTFT	NYCMH	WVRQDHQAQGLEWMG
QVQLQESGPGLVKpSETLSLYCAVSGDSIS	SGNW*I	WVRQPPGKGLEWIG
GPRLEASETLSLCTVSGGSIS	SSYYW	WIRQPPGKGLEWIG
QVQLQESGPGLVKpSETSLTCAVYGGSF	SYWS	WIRQPPGKGLEWIG
LSLICAVSGSSIS	SGNW*I	WVRQPPGKGLEWIG
SETLSLTCAVYGGSF	GYWS	WIRQPPGKGLEWIG
SRAQTGEASETLSLCTVSGGSIS	SSYYWG	WVRQPPGKGLEWIG
CPLTCTVSGGSVSSGS	YYWS	WIRQPPGKGLEWIG
GLVKPSETLSLCTVSGGSIS	SYWS	WIGSPPGKGLEWIG
SFETLSLICAVSGDSIS	SGNW*I	WVRQPPGKGLEWIG
QVQLVQSGAEVKPGSSVKVSCKASGGTFS	SYAIS	WVRQAPGQGLEWMG
QVOLQWAGAGLLKPSETSLTCAVYGGSF	GYWS	WIRQPPGKGLEWIG
QIQLQESGPGLVKPSETLSLCTVSGGSIS	SSYYWG	WIRQPPGKGLEWIG
GPGLVKPSQTLSTCTVSGGSIS	SGGYYWS	WIRQNPNGKGLEWIG

* indicates stop codon (unsure as sequence remains in frame)
 • sequence terminates due to internal restriction site
 lower case denotes frame shift

CDR2	FR3	CDR3
WISAYNGNTNYAQKLOG	RVTIMTDTSSTAYMELRSRLSDDTAVYYCAR	DTVSS
WINAGNGNTKYQKLOG	RVTITRDTSASTAYMOLSSLRSEDTAVYYCAR	DTVSS
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS•	
RIYTSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSVTAAADTAVYYCAR	DTVSS
LVCPSDGSTSAYQKFQA	RVTITRDTSMSTAYMELSSLRSEDTAMYYCAR	DTVSS
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS•	
EINHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLS•	
YIYYSGSTNYNPSLKS	RVTISVDTSKNQFSLKLS•	
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS•	
EINHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSVTAAADTAVYYCAR	DTVSS
LVCPSDGSTSAYQKFQA	RVTITRDTSMSTAYMELSSLRSEDTAMYYCAR	DTVSS
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS•	
SIYYSGSTYYNPSLKS	RVTIPVDTSKNQFSLKLS•	
YIYYSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSVTAAADTAVYYCAR	DTVSS
RIYTSGSTNYNPSLKS	RVTMSVDTSKNQFSLKLS•	
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS•	
RIIPILGIANYAQKFQG	RVTITADKSTSTAYMELSSLRSEDTAVYYCAR	DTVS
EINHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLS•	
EINHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLS•	
YIYYSGSTYYNPSLKS	RVTISVDTSKNQFSLKLSVTAAADTAVYYCAR	DTVSS

FIG. 12

psw1

HindIII site AAGCTT

M K Y L L P T A A

GCATGCAAATTCTATTCAGGAGACAGTCATAATGAAATACCTATTGCCATCGGCAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q E S
 GCTGGATTGTTATTACTCGCTGCCAACCCAGCGATGGCCCAGGTGCAGCTGCAGGAGTC
 70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
 GGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
 130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAACCGCTATGGTGTAACTGGGTTGCAGCCTCCAGGAAGGGCTGGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
 CTGGGAATGATTGGGGTGTGGAAACAGACTATAATTCTAGCTCTAAATCCAGACTG
 250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTTCTTAAAAATGAACAGTCGTGACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
 GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGA
 370 380 390 400 410 420

FIG. 13

PSW2

HindIII AAGCTT

	M	K	Y	L	L	P	T	A	A
GCATGCAAATTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC									
10	20	30	40	50	60				

A	G	L	L	L	A	A	Q	P	A	M	A	Q	V	Q	L	Q	E	S
GCTGGATTGTTATTACTCGCTGCCAACAGCGATGGCCAGGTGCAGCTGCAGGAGTC																		
70	80	90	100	110	120													

G	P	G	L	V	A	P	S	Q	S	L	S	I	T	C	T	V	S	G	F
GGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC																			
130	140	150	160	170	180														

S	L	T	G	Y	G	V	N	W	V	R	Q	P	P	G	K	G	L	E	W
TCATTAACCGGTATGGTGTAAACTGGGTGCCCCAGCTCCAGGAAGGGTCTGGAGTGG																			
190	200	210	220	230	240														

L	G	M	I	W	G	D	G	N	T	D	Y	N	S	A	L	K	S	R	L
CTGGGAATGATTGGGTGATGGAAACACAGACTATAATTAGCTCTCAAATCCAGACTG																			
250	260	270	280	290	300														

S	I	S	K	D	N	S	K	S	Q	V	F	L	K	M	N	S	L	H	T
AGCATCAGCAAGGACAACCTCAAGAGCCAAGTTCTAAAAATGAACAGTCTGCACACT																			
310	320	330	340	350	360														

D	D	T	A	R	Y	Y	C	A	R	E	R	D	Y	R	L	D	Y	W	G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTACTGGGC																			
370	380	390	400	410	420														

Q	G	T	T	V	T	V	S	S											
CAAGGCACCACGGTCACCGTCTCCTCATATAAGAGCTGAATTGCCAAGCTTGCATGC																			
430	440	450	460	470	480														

M	K	Y	L	L	P	T	A	A	A	;									
AAATTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCCTGGA																			
490	500	510	520	530	540														

L	L	L	A	A	Q	P	A	M	A	D	I	V	L	T	Q	S	P	A	
TTGTTATTACTCGCTGCCAACAGCGATGGCCGACATCGCTCTGACTCAGTCTCCAGCC																			
550	560	570	580	590	600														

S	L	S	A	S	V	G	E	T	V	T	I	T	C	R	A	S	G	N	I
TCCCTTCTGCCCTGTGGAGAAAAGTCACCATCACATGTCGAGCAAGTGGGAATT																			
610	620	630	640	650	660														

H	N	Y	L	A	W	Y	Q	Q	K	Q	G	K	S	P	Q	L	L	V	Y
CACAATTATTTAGCATGGTATCAGCAGAACAGGGAAAATCTCCTCAGCTCCTGGCTAT																			
670	680	690	700	710	720														

FIG. 14a

```

Y T T T L A D G V P S R F S G S G S G T
TATACAACAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAAGGTCAGTGGCAGTGGATCAGGAACA
730      740      750      760      770      780

Q Y S L K I N S L Q P E D F G S Y Y C Q
CAATATTCTCTCAAGATCAACAGCCTGCAACCTGAAGATTTGGGAGTTATTACTGTCAA
790      800      810      820      830      840

H F W S T P R T F G G G T K L E I K R
CATTTTGAGTACTCCTCGGACGTTGGAGGCACCAAGCTGGAAATCAAACGGTAA
850      860      870      880      890      900

TAAGAGCTCGAATT
910

```

FIG. 14 b

pSW1HPOLMYC

HindIII site AAGCTT

```

M K Y L L P T A A
GCATGCAAATTCTATTCAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10      20      30      40      50      60

A G L L L L A A Q P A M A Q V Q L Q
GCTGGATTGTTATTACTCGCTGCCAACAGCGATGGCCAGGTGCAGCTGCAG
70      80      90      100     110 PstI

```

Polylinker

TCTAGA GTCGAC CTCGAG

XbaI SalI XhoI

MYC PEPTIDE

V T V S S E O K L I S E E D L N * *

GGTCACCGTCTCCTCAGAACAAAAACTCATCTCAGAAGAGGATCTGAATTAATAA

BstEII

GGGCTAAGCTCGAATT

FIG. 15

1 VH3 QVQLQESGPELVKPGASVKMSCKASGYTFT VH8 QVQLQESGPELVKPGASVKMSCKASGYTFT VH-D1.3 QVQLKESGPGLVAPSQSLSITCTVSGFSLT	CDR1 SYVMH SYVMH GYGVN	49 WVKQKPGAGLEWIG WVKQKPGQGLEWIG WVRQPPGKGLEWLG
50 VH3 YINPYNDGKYNEKFKG VH8 YINPYNDGSKYNEKFKG VH-D1.3 MIW GDGNTDYNALKS	CDR2 KATLTSOKSSSTAYMELSSLTSEDSAVYYCAV KATLTADKSSNTAYMQLSSLTSEDSAVYYCAR RLSISKDNSKSQVFLKMNSLHTDDTARYYCAR	94
95 CDR3 VH3 LLLRYFFDY VH8 GAVVSYYAMDY VH-D1.3 ERDYRLDY	113 WGQGTTTVVSS WGQGTTTVVSS WGQGTTTVVSS	

FIG. 16

FR1 QVQLQESGGGLVQPGGSLRLSCAASGFTFS SYAMS	CDR1
FR2 WVRQAPGKGLEWVS	
AISGSGGSTYYADSVKG	CDR2
FR3 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAM WRGIATPVSFDLGYFDY	CDR3

FIG. 17

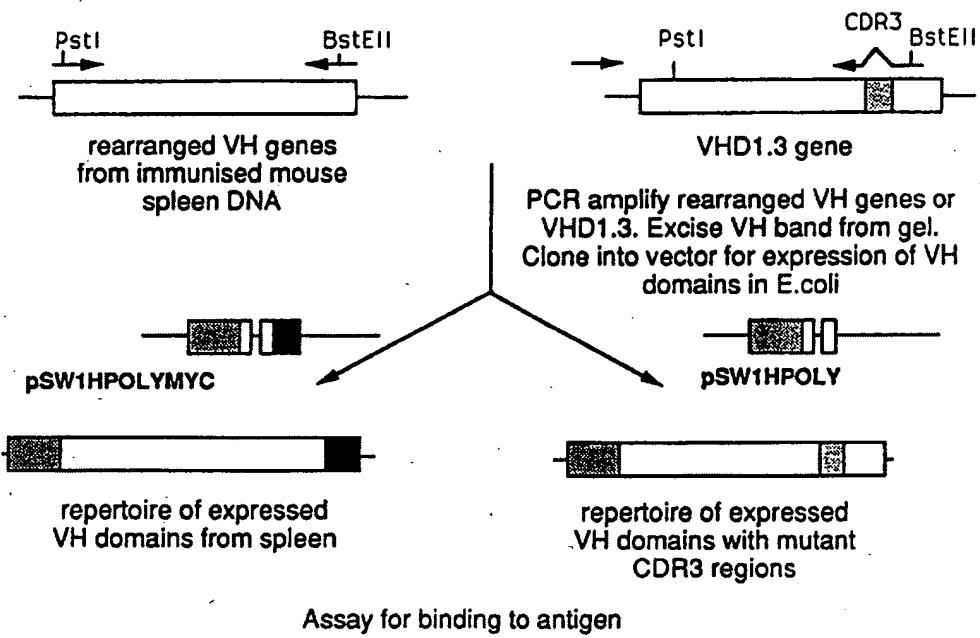


FIG. 18

pSW2HPOLY

HindIII AAGCTT

	M	K	Y	L	L	P	T	A	A
GCATGCAAATTCTATTC	A	G	A	G	A	C	T	A	A
10	20	30	40	50	60				

A	G	L	L	L	A	A	Q	P	A	M	A	Q	V	Q	L	Q
GCTGGATTGTTATTACTCGCTGCCAACCAGCGATGGCCAGGTGCAGCTGCAG	70	80	90	100	110	PstI										

TCTAGA GTCGAC CTCGAG
XbaI SalI XhoI

V	T	V	S	S												
GGTCACCGTCTCCTCATATAAGAGCTCGAATTGCCAACGCTTGATGC	BstEII	430	440	450	460	470	480									

M	K	Y	L	L	P	T	A	A	A	G						
AAATTCTATTC	A	G	G	A	C	G	T	C	A	C	GGC	3GA				
490	500	510	520	530	540											

L	L	L	A	A	Q	P	A	M	A	D	I	V	L	T	Q	S	P	A
TTGTTATTACTCGCTGCCAACCGCGATGGCCGACATCGCTGACTCAGTCTCCAGCC	550	560	570	580	590	600												

S	L	S	A	S	V	G	E	T	V	T	I	T	C	R	A	S	G	N	I
TCCCTTCTCGCTCTGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATTATT	610	620	630	640	650	660													

H	N	Y	L	A	W	Y	Q	Q	K	Q	G	K	S	P	Q	L	L	V	Y
CACAATTATTAGCATGGTATCAGCAGAACAGGGAAAATCCTCTAGCTCTGGTCTAT	670	680	690	700	710	720													

Y	T	T	T	L	A	D	G	V	P	S	R	F	S	G	S	G	S	G	T
TATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTTCAAGTCAGTGGCAGTGGATCAGGAACA	730	740	750	760	770	780													

Q	Y	S	L	K	I	N	S	L	Q	P	E	D	F	G	S	Y	Y	C	Q
CAATATTCTCTCAAGATCAACAGCCTGCAACCTGAAGATTGGAGTTATTACTGCAA	790	800	810	820	830	840													

H	F	W	S	T	P	R	T	F	G	G	G	T	K	L	E	I	K	R
CATTTTGAGTACTCCTCGGACGTTGGTGGAGGCACCAAGCTGGAAATCAAACGGTAA	850	860	870	880	890	900												

TAAGAGCTCGAATT
910

FIG. 19

	M	K	Y	L	L	P	T
AAGCTTGCATGCAAATTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACG	10	20	30	40	50	60	
AAAAGL L L L A A Q P A M A Q V Q L Q	70	80	90	100	110	120	
E S G P G L V A P S Q S L S I T C T V S	130	140	150	160	170	180	
GAGTCAGGACCTGGCTGGTGGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCA							
G F S L T G Y G V N W V R Q P P G K G L	190	200	210	220	230	240	
GGGTTCTCATTAACCGGCTATGGTGAAACTGGGTTGCCAGCCTCCAGGAAAGGGTCTG							
E W L G M I W G D G N T D Y N S A L K S	250	260	270	280	290	300	
GAGTGGCTGGGAATGATTGGGTGATGAAACACAGACTATAATTAGCTCTCAAATCC							
R L S I S K D N S K S Q V F L K M N S L	310	320	330	340	350	360	
AGACTGAGCATCAGCAAGGACAACCTCAAGAGCCAAGTTTCTTAAAAATGAAACAGTCTG							
H T D D T A R Y Y C A R E R D Y R L D Y	370	380	390	400	410	420	
CACACTGATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTAGGCTTGACTAC							
W G Q G T T V T V S S G G G A P A A A P	430	440	450	460	470	480	
TGGGGCCAAGGCACCACGGTCACCGTCTCCTCAGGTGGTGGTGCCTCAGCAGCTGCACCT							
A G G G Q V Q L K E S G P G L V A P S Q	490	500	510	520	530	540	
GCTGGAGGAGGACAGGTGCAGCTGAAGGAGTCAGGACCTGGCTGGTGGCGCCCTCACAG							
S L S I T C T V S G F S L T G Y G V N W	550	560	570	580	590	600	
AGCCTGTCATCACATGCACCGTCTCAGGGTTCTCATTAACCGGCTATGGTGAAACTGG							
V R Q P P G K G L E W L G M I W G D G N	610	620	630	640	650	660	
GTTCGCCAGCCTCCAGGAAAGGGCTGGAGTGGCTGGGAATGATTGGGTGATGGAAAC							
T D Y N S A L K S R L S I S K D N S K S	670	680	690	700	710	720	
ACAGACTATAATTAGCTCTCAAATCCAGACTGAGCATCAGCAAGGACAACCTCAAGAGC							
Q V F L K M N S L H T D D T A R Y Y C A	730	740	750	760	770	780	
CAAGTTTCTTAAAAATGAAACAGTCTGCACACTGATGACACAGCCAGGTACTACTGTGCC							
R E R D Y R L D Y W G Q G T T V T V S S	790	800	810	820	830	840	
AGAGAGAGAGATTAGGCTTACTACTGGGCCAAGGCACCAAGGTACCGTCTCCTCA							
*	*						
TAATAAGAGCTC							
850							

FIG. 20

M K Y L L P T A A
 GCATGCAAATTCTATTCAGGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
 10 20 30 40 50 60

A G L L L A A Q P A M A Q V Q L Q E S
 GCTGGATTGTTATTACTCGCTGCCAACCGCGATGGCCAGGTGCAGCTGCAGGAGTCA
 70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
 GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
 130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
 TCATTAACCGGCTATGGTCTAAACTGGGTTGCCAGCCTCCAGGAAAGGGTCTGGAGTGG
 190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
 CTGGGAATGATTGGGGTGATGGAAACACAGACTATAATTAGCTCTCAAATCCAGACTG
 250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
 AGCATCAGCAAGGACAACCCAAGAGCCAAGTTCTAAAAATGAACAGTCTGCACACT
 310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
 GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTACTGGGGC
 370 380 390 400 410 420

Q G T T V T V S S R T P E M P V L E N R
 CAAGGCACCACGGTCACCGTCTCCTCACGGCACCCAGAAATGCCCTGTTCTGGAAAACCGG
 430 440 450 460 470 480

A A Q G D I T A P G G A R R L T G D Q T
 GCTGCTCAGGGCGATATTACTGCACCCGGCGGTGCTCGCCGTTAACGGGTGATCAGACT
 490 500 510 520 530 540

A A L R D S L S D K P A K N I I L L I G
 CGCGCTCTGCGTGATTCTCTTAGCGATAAAACCTGCAAAAATATTATTTGCTGATTGGC
 550 560 570 580 590 600

D G M G D S E I T A A R N Y A E G A G G
 GATGGGATGGGGACTCGGAAATTACTGCCGACGTAATTATGCCGAAGGTGCGGGCGGC
 610 620 630 640 650 660

F F K G I D A L P L T G Q Y T H Y A L N
 TTTTTAAAGGTATAGATGCCTTACCGCTTACCGGGCAATACACTCACTATGCGCTGAAT
 670 680 690 700 710 720

K K T G K P D Y V T D S A A S A T A W S
 AAAAAGGCAACCGGACTACGTACCGACTCGGCTGCATCAGCAACCGCCTGGTCA
 730 740 750 760 770 780

FIG. 21a

T G V K T Y N G A L G V D I H E K D H P
 ACCGGTGTCAAAACCTATAACGGCGCTGGCGTCGATATTACGAAAAAGATCACCA
 790 800 810 820 830 840

T I L E M A K A A G L A T G N V S T A E
 ACGATTCTGAAATGGAAAAGCCGCAGGTCTGGCAGCGTAACGTTCTACCGCAGAG
 850 860 870 880 890 900

L Q D A T P A A L V A H V T S R K C Y G
 TTGCAGGATGCCACGCCGCTGCGCTGGCACATGTGACCTCGCGAAATGCTACGGT
 910 920 930 940 950 960

P S A T S E K C P G N A L E K G G K G S
 CCGAGCGCACCAGTAAAAATGTCGGGTAACGCTCTGGAAAAAGCCGAAAGGATCG
 970 980 990 1000 1010 1020

I T E Q L L N A R A D V T L G G G A K T
 ATTACCGAACAGCTGCTTAACGCTCGTGCCGACGTTACGCTTGGCGCGCAAAC
 1030 1040 1050 1060 1070 1080

F A E T A T A G E W Q G K T L R E Q A Q
 TTTGCTGAAACGGCAACCGCTGGTGAATGGCAGGGAAAACGCTGCGTGAACGGCACAG
 1090 1100 1110 1120 1130 1140

A R G Y Q L V S D A A S L N S V T E A N
 GCGCGTGGTTACAGTTGGTGAGCGATGCTGCCACTGAATTGGTACGGAAAGCGAAT
 1150 1160 1170 1180 1190 1200

Q Q K P L L G L F A D G N M P V R W L G
 CAGCAAAACCCCTGCTGGCCTGTTGCTGACGGCAATATGCCAGTGGCTGGCTAGGA
 1210 1220 1230 1240 1250 1260

P K A T Y H G N I D K P A V T C T P N P
 CCGAAAGGAAACGTACCATGGCAATATCGATAAGCCCGCAGTCACCTGACGCCAAATCCG
 1270 1280 1290 1300 1310 1320

Q R N D S V P T L A Q M T D K A I E L L
 CAACGTAATGACAGTGTACCAACCCCTGGCGCAGATGACCGACAAAGCCATTGAATTGTTG
 1330 1340 1350 1360 1370 1380

S K N E K G F F L Q V E G A S I D K Q D
 AGTAAAAATGAGAAAGGTTTCTGCAAGTTGAAGGTGGCTCAATCGATAAACAGGAT
 1390 1400 1410 1420 1430 1440

H A A N P C G Q I G E T V D L D E A V Q
 CATGCTGCGAATCCTGTGGCAAATTGGCGAGACGGTCAATCGATAAACAGGAT
 1450 1460 1470 1480 1490 1500

R A L E F A K K E G N T L V I V T A D H
 CGGGCGCTGGAATTGCTAAAAAGGAGGGTAACACGCTGGTCATAGTCACCGCTGATCAC
 1510 1520 1530 1540 1550 1560

FIG. 21b

A H A S Q I V A P D T K A P G L T Q A L
GCCACGCCAGCCAGATTGTTGCCCGGATACCAAAGCTCCGGGCCTCACCCAGGGCTA
1570 1580 1590 1600 1610 1620

N T K D G A V M V M S Y G N S E E D S Q
AATACCAAAGATGGCGCAGTGATGGTGATGAGTTACGGAACTCCGAAGAGGATTCAAA
1630 1640 1650 1660 1670 1680

E H T G S Q L R I A A Y G P H A A N V V
GAACATACCGGCAGTCAGTGCCTATTGCGGTATGGCCCGCATGCCGCCATGTTGTT
1690 1700 1710 1720 1730 1740

G L T D Q T D L F Y T M K A A L G L K *
GGACTGACCGACCAGACCGATCTTCTACACCATGAAAGCCGCTCTGGGGCTGAATAA
1750 1760 1770 1780 1790 1800

AACCGCGCCCGGGAGTGAATTCGCTGCCGGGTGGTTTTGCTGTTAGC
1810 1820 1830 1840 1850

FIG. 21c

M K Y L L P T A A A
 GCATGCAAATTCTATTCAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
 10 20 30 40 50 60

A G L L L A A Q P A M A Q V Q L Q E S
 GCTGGATTGTTATTACTCGCTGCCAACCGCGATGGCCAGGTGCAGCTGCAGGAGTCA
 70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
 GGACCTGGCCTGGTGGCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
 130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
 TCATTAACCGGCTATGGTGTAAACTGGGTTGCCAGCCTCAGGAAAGGGTCTGGAGTGG
 190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
 CTGGGAATGATTGGGTGATGAAACACAGACTATAATTCTAGCTCTCAAATCCAGACTG
 250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
 AGCATCACCAAGGACAACCCAAGAGCCAAGTTCTAAAAATGAACAGTCTGCACACT
 310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
 GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTACTGGGGC
 370 380 390 400 410 420

Q G T T V T V S S * *
 CAAGGCACCAAGGTACCGTCTCCTCATAATAAGAGCTATCCGGAGCTTGCATGCAA
 430 440 450 460 470 480

M K Y L L P T A A A A G L
 TTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTG
 490 500 510 520 530 540

L L L A A Q P A M A D I E L V D L E I K
 TTATTACTCGCTGCCAACCGCGATGGCCGACATCGAGCTCGTCGACCTCGAGATCAA
 550 560 570 580 590 600

R E Q K L I S E E D L N * *
 CGGGAACAAAAACTCATCTCAGAAGAGGATCTGAATTAATAATGATCAAACGGTAATAAG
 610 620 630 640 650 660

GATCCAGCTCGAATTC
 670

FIG. 22

A

Q	V	Q	L	Q	E	S	G	P	G	L	V	Q	P	S	Q	S	L	S	I
CAGGTGCAGCTGCAGGAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATC																			
10	20	30	40	50	60														
T	C	T	V	S	G	F	S	L	T	S	Y	G	V	H	W	V	R	Q	S
ACCTGCACAGTCTCTGGTTCTCATTAACTAGCTATGGTGTACACTGGGTTGCCAGCTC																			
70	80	90	100	110	120														
G			N											P					
P	G	K	G	L	E	W	L	G	M	I	W	G	D	G	N	T	D	Y	N
CCAGGAAAGGGTCTGGAGTGGCTGGGAATGATTGGGGTGATGGAAACACAGACTATAAT																			
130	140	150	160	170	180														
S	A	L	K	S	R	L	S	I	S	K	D	N	S	K	S	Q	V	F	L
TCAGCTCTCAAATCCAGACTGAGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTCTTA																			
190	200	210	220	230	240														
K	M	N	S	L	H	T	D	D	T	A	R	Y	Y	C	A	R	E	R	D
AAAATGAACAGTCTGCACACTGATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAT																			
250	260	270	280	290	300														
Y	R	L	D	Y	W	G	Q	G	T	T	V	T	V	S	S				
TATAGGCTTGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA																			
310	320	330	340																

FIG. 23